

	414605	1465790_1	BE390440
	415747	155189_1	AA381209 AA381245 AA167683
	416173	1574973_1	R52782 R17313 H24192 R19876
5	417742	1696282_1	R64719 Z44680 R12451
	417974	171237_1	AA210765 T95700 H94407
	418636	177402_1	AW749855 AA225995 AW750208 AW750206
	419536	185688_1	AA603305 AA244095 AA244183
	420854	197072_1	AW296927 AI684514 AI263168 AA281079
10	422156	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643
			AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
	422986	223666_1	BE091089 BE091123 AA319959
	423833	232451_1	AW503329 N46610 AA331571
	423841	232507_1	AW753967 AA370795 AA331630 AW962550
15	423945	233566_1	AA410943 AW948953 AA334202 AA332682
	425201	247933_1	AA352111 AW982247 AA429695
	426650	270283_1	AA382614 AA402411 AA412355
	426878	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
	430264	315008_1	AA470519 BE303010 BE302954 BE384120
20	430785	323486_1	Z30201 AA486132 T72025
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
	433687	373061_1	AA743991 AA604852 AW272737
	434338	383982_1	AW754311 AA630185 AW803285
	434469	387447_1	AA634806 C18732 AA729161 AA729860
	435447	406400_1	AI872932 AA682306 BE220163 W88695 TB1307 H91447
25	437152	43386_1	AL050027 BE086051
	437854	44418_1	AL119723 AL119874 AI809018 U50537
	439031	46798_1	AF075079 H48601 H48795
	439255	470321_1	BE164500 AA832198 BE164502
	444910	624951_1	AI201849 BE089007 AW946544
30	445432	63943_1	AV653771 BE089370
	446922	69865_1	BE175605 Z43529 F06610 BE175602 AV661027
	447197	711623_1	R36075 AI366546 R36167
	448420	76273_1	BE623004 AA380669 BE263627 BE246433
35	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	450522	837264_1	AI698839 AI809260 AI909259
	450736	844552_1	AW970060 AI732366 AI792313 AW839644
	451024	85565_1	AA442176 AA259181
	451067	85759_1	BE172186 AA059279 AA020815 AA013437
40	451340	86640_1	AW936273 AW340350 AA017208
	452542	921410_1	AW812256 AW812257 AI906423 AI906422
	452564	92227_1	AA026777 N50065 R09961 N54721
	453472	968371_1	AL037925 AL037931 AL037957
	454307	1106070_1	AW855717 AW362452 AW362443
	454359	1130674_1	N71277 AW390764
45	454545	1223779_1	AW806899 AW866451 AW866393 AW866297 AW817889
	454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	454714	1230493_1	AW815098 BE154843 BE154831
	455047	1250536_1	AW852530 AW852527 AW852526
	455092	1252971_1	BE152428 AW855572 AW855607
50	455097	1253130_1	AW855802 AW855794 AW855797 AW855806 AW855796 AW855808 AW855793 AW855807
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW8561034
	455431	1289854_1	AW938484 BE001245 BE001190
	455511	1321229_1	BE144762 AW979091
	455609	1337548_1	BE011668 BE011689 BE011627 BE011679 BE011699 BE011678 BE011696 BE011675 BE011622 BE011635
55	455651	1348732_1	BE064952 BE064979 BE064853 BE064857 BE064856 BE064977 BE064980 BE064860 BE064815 BE064957 BE064804
			BE064816 BE064850 BE064805 BE064796 BE064818 BE064975 BE064819 BE064810 BE064668 BE065059
	455685	1350393_1	BE066976 BE066928 BE066927
	455700	1351264_1	BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
	455708	1352232_1	BE069326 BE069290 BE069352
60	455732	1353874_1	BE080908 BE072258 BE072190 BE072236
	455838	1374605_1	BE145808 BE145807 BE181883
	455935	1384144_1	BE158687 BE158688
	455945	1385588_1	BE160638 BE160606 BE160703
	456207	165078_1	AA193450
65	456482	192289_1	AA485224 AA287308 AA258121
	458094	47311_1	AF086325 W72956 W73221 AA219112
	458673	679507_1	N99626 AI302701

TABLE 19B

5 **Table 19B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 19. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 15 Nt\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
20	400555	9801191	Minus	134694-134817
	400608	9887666	Minus	96756-97558
	400610	9887671	Minus	117606-117928,124040-124147
	400925	7651921	Plus	38183-38391,43900-44086
	401045	8117619	Plus	90044-90184,91111-91345
	401049	7232177	Plus	149157-150692
25	401093	8516137	Minus	22335-23166
	401256	9796573	Minus	45482-45620
	401283	9800093	Minus	47256-47456
	401326	9212516	Minus	226246-227505
	401418	7452889	Minus	124865-125075
30	401451	6634068	Minus	119926-121272
	401458	9187886	Plus	76485-77597
	401497	7381770	Plus	92607-92813
	401508	7534110	Minus	110779-110983
	401575	7229804	Minus	76253-76364
35	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401793	7283888	Minus	102945-103083
40	401987	4406829	Minus	72893-73021,76938-77049
	402077	8117414	Plus	65014-65195
	402109	8131678	Minus	171722-171859,173197-173303
	402184	8576001	Minus	112644-112986,113505-113636
	402376	9625329	Minus	21753-22385
45	402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
	402578	9884928	Plus	66350-66496
	402608	9909429	Minus	81747-82094
	402696	7328818	Minus	23600-23731
	402765	9367757	Plus	109588-109726
50	402800	6010175	Plus	43921-44049,46181-46273
	402820	6456853	Minus	82274-82443
	402892	8086844	Minus	194384-194645
	403133	7331427	Plus	38314-38634
	403356	6569930	Plus	92839-93036
55	403388	9438331	Plus	112733-113001,114599-114735
	403426	9719529	Minus	157156-158183
	403585	8101208	Minus	131266-131769
	403593	6862650	Minus	62554-62712,69449-69602
	403637	8671936	Minus	142647-142771,145531-145762
60	403639	8671948	Plus	113234-113326,115186-115287,119649-119786
	403677	7331517	Minus	55008-55083,62860-63051
	403775	7770580	Minus	102247-102326,103095-103148
	403943	7711864	Plus	100742-100904,101322-101503

	404091	7684554	Minus	82121-83229
	404097	7770701	Plus	55512-55781
	404142	9856692	Minus	80316-80459
	404253	9367202	Minus	55675-56055
5	404274	9885189	Plus	104127-104318
	404285	2326514	Plus	32282-32416
	404360	9858450	Minus	122873-122966,151324-151469,153093-153253
	404440	7528051	Plus	80430-81581
	404443	7579073	Minus	87198-87441
10	404552	7243881	Plus	19854-20010
	404561	9795980	Minus	69039-70100
	404580	6539738	Minus	240588-241589
	404721	9856648	Minus	173763-174294
	404828	6572184	Plus	47726-48046
15	404983	4432779	Minus	51178-51374,52000-52173
	405037	7543748	Minus	127374-127578
	405041	7547195	Plus	121230-121714
	405095	8072599	Plus	138877-139066
	405153	9965565	Minus	176317-175500
20	405196	7230083	Minus	135716-135851
	405232	7249042	Plus	125904-126063
	405248	7259728	Plus	637-777
	405336	6094635	Plus	33267-33563
	405394	6624123	Minus	31900-32373
25	405460	7684569	Minus	52223-52389
	405494	8050952	Minus	70284-70518
	405547	1054740	Plus	124361-124520,124914-125050
	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-48554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
30	405638	6289229	Plus	199260-199372,199826-199929
	405654	4895155	Minus	53624-53759
	405718	9795467	Plus	113080-113266
	405822	6273498	Minus	154680-154974,155203-155379
	405848	7651809	Minus	28135-28244
35	405873	6758747	Minus	32129-32764
	405906	7705124	Minus	10835-11059
	405917	7712162	Minus	106829-107213
	405925	6758795	Plus	129935-130282
	405953	7960374	Minus	65101-65574
40	406069	9117732	Plus	68880-69374
	406151	7144806	Minus	94087-94285
	406153	9929734	Minus	12902-13069
	406182	5923650	Minus	28256-28935
	406271	7534217	Plus	36179-36692
45	406291	5686274	Plus	9562-9867
	406348	9255985	Minus	71754-71944
	406414	9256407	Plus	49593-49850
	406446	9454509	Minus	116424-116527,118721-118859,121187-121364
	406504	7711360	Minus	107068-107277
50	406554	7711566	Plus	106956-107121

**TABLE 20: 544 GENES UP-REGULATED IN BREAST CANCER  
COMPARED TO NORMAL ADULT TISSUES THAT ARE  
LIKELY TO ENCODE EXTRACELLULAR OR CELL-  
SURFACE PROTEINS**

Table 20 shows 544 genes up-regulated in breast cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the "average" normal adult tissue level was set to the 85<sup>th</sup> percentile value amongst 144 non-malignant tissues, and the 96<sup>th</sup> percentile value amongst the 73 breast cancer specimens was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigenID: Unigene number  
Pred.Prot.Domains: Predicted Protein Domains  
Unigen Title: Unigene gene title  
R1: Ratio of 93<sup>rd</sup> percentile of tumor to 85<sup>th</sup> percentile of normal body tissue

Pkey	ExAccn	UnigenID	Pred.Prot.Domains	UnigenTitle	R1
408591	AF015224	Hs.46452	SS,Uterogloblin,SS,Uterogloblin	mammaglobin 1	168.6
400291	AA401369	Hs.190721	TM	ESTs	73.2
449746	A1668594	Hs.176588	,SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	65.7
407277	AW170035	Hs.326736	TM	Homo sapiens breast cancer antigen NY-BR	57.6
400292	AA250737	Hs.72472	death,ZU5,TM,Activin_recp,kinase,	BMP-R1B	55.9
424735	U31875	Hs.272499	,SS,TM	short-chain alcohol dehydrogenase family	53.8
426876	BE069341		TM	gb:QV3-BT0381-270100-073-c08 BT0381 Homo	50.3
428848	NM_000230	Hs.194236	SS,Leptin,SS,Leptin,	leptin (murine obesity homolog)	40.8
407178	AA195651	Hs.104106	,SS,Dihydroorotase,	ESTs	39.3
409000	L11690	Hs.620	Plectin_repeat,SH3,spectrin,SS,Plectin_r	bullous pemphigoid antigen 1 (230/240kD)	37.3
427585	D31152	Hs.179729	SS,C1q,Collagen,SS,C1q,Collagen,	collagen, type X, alpha 1 (Schmid metaph	35.2
429441	AJ224172	Hs.204096	,SS,Uterogloblin,	lipophilin B (uterogloblin family member)	30.0
450375	AA009647	Hs.8850	,SS,TM,disintegrin,Pep_M12B_propep,Repro	a disintegrin and metalloproteinase doma	25.7
420931	AF044197	Hs.100431	SS,IL8,SS	small inducible cytokine B subfamily (Cy	25.2
422109	S73265	Hs.1473	SS,Bombesin,SS	gastrin-releasing peptide	24.8
445730	A1624342	Hs.170042	,SS,TM,Cation_efflux	ESTs	24.1
451110	A1955040	Hs.265398	SS	ESTs, Weakly similar to transformation-r	24.0
400297	A1127076	Hs.334473	TM	hypothetical protein DKFZp564O1278	23.8
420813	X51501	Hs.99949	SS,SS	prolactin-induced protein	22.8
452744	A1267652	Hs.30504	,SS,TM,GNS1_SUR4,cNMP_binding,Rila	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	22.6
424634	NM_003613	Hs.151407	lg,tsp_1,SS,AAA	cartilage intermediate layer protein, nu	21.7
420757	X78592	Hs.99915	hormone_rec,Androgen_recep,zf-C4,	androgen receptor (dihydrotestosterone r	21.7
424399	A1905687	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	20.3
447350	A1375572	Hs.172634	,kinase,	ESTs	19.2
456207	AA193450		,SS,TM,p450,p450	gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	18.3
431448	AL137517	Hs.334473	TM	hypothetical protein DKFZp564O1278	18.2
427217	AA399272	Hs.144341	SS	ESTs	18.2
456938	X52509	Hs.161640	,SS,TM,aminotran_1_2,Cadherin_C_term,cad	tyrosine aminotransferase	18.1
435496	AW840171	Hs.265398	SS	ESTs, Weakly similar to transformation-r	17.9
402578			SS,p450,SS,TM,p450	C1001134:g 2117372 pir  65981 fatty ac	17.8
453160	A1263307	Hs.239884	SS	H2B histone family, member L	17.8
422505	AL120862	Hs.124165	SS	programmed cell death 9 (PDCD9)	17.7
444342	NM_014398	Hs.10887	Lamp,SS,TM,Lamp,	similar to lysosome-associated membrane	17.5

	449765	N92293	Hs.206832	SS	ESTs, Moderately similar to ALU8_HUMAN A	17.3
	428227	AA321649	Hs.2248	SS,IL8,	small Inducible cytokine subfamily B (CX	17.0
	425692	D90041	Hs.155956	,SS,Acetyltransf2,	N-acetyltransferase 1 (arylamine N-acety	16.7
	424001	W67883	Hs.137476	,pkinase,	paternally expressed 10	16.5
5	448595	AB014544	Hs.21572	LRRCT,LRR,SS,LRRCT,serine_carbpept	KIAA0544 gene product	16.3
	449448	D60730	Hs.57471	SS	ESTs	16.2
	418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10,SS,Peptidase	matrix metalloproteinase 1 (MMP1; inters	15.7
	418994	AA296520	Hs.89546	SS,lectin_c,sushi,EGF,SS,EGF,lectin_c,su	selectin E (endothelial adhesion molecu	15.5
10	453596	AA441838	Hs.82905	SS	hypothetical protein FLJ14834	15.5
	452401	NM_007115	Hs.29352	,SS,CUB,Xlink,	tumor necrosis factor, alpha-induced pro	15.0
	446591	H44186	Hs.15456	PDZ,SS	PDZ domain containing 1	14.9
	419296	AA236115	Hs.120785	SS	ESTs	14.8
	452838	U65011	Hs.30743	SS,SS	preferentially expressed antigen in mela	14.7
15	422805	AA436989	Hs.121017	histone,SS,histone,histone	H2A histone family, member A	14.3
	448390	AL035414	Hs.21068	SS	hypothetical protein	14.2
	447342	AI199268	Hs.19322	,SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 2010	14.2
	411869	W20027	Hs.23439	,SS,Peptidase_M1,	ESTs	13.9
	443709	AI082692	Hs.134662	,SS,TM,SNF	ESTs	13.7
	459587	AA031956		,SS,LIM,	gb:z15e04.s1 Soares_pregnant_uterus_NbH	13.7
20	442580	AI733682	Hs.130239	SS	ESTs	13.5
	400269	X07820	Hs.2258	hemopexin,Peptidase_M10,SS,Peptidase_M10	matrix metalloproteinase 10 (MMP10; str	13.5
	411598	BE336654	Hs.70937	histone,SS,histone,histone	H3 histone family, member A	13.3
	415263	AA948033	Hs.130853	,SS,histone,histone,linker_histone	ESTs	13.2
	433805	AA706910	Hs.112742	,SS,Ribosomal_L7Ae,	ESTs	13.1
25	407276	AI951118	Hs.326736	TM	Homo sapiens breast cancer antigen NY-BR	13.1
	443348	AW873598	Hs.182278	,SS,DENN	calmodulin 2 (phosphorylase kinase, delt	13.0
	421037	AI684808	Hs.197653	SS	programmed cell death 9 (PDCD9)	12.9
	424086	AI351010	Hs.102267	,SS,Lysyl_oxidase	lysyl oxidase	12.8
	400295	W72838	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	12.7
30	452461	N78223	Hs.108106	,SS,G9a,PHD,	transcription factor	12.5
	427365	AI873274	Hs.190721	TM	ESTs	12.4
	433365	AF026944	Hs.293797	,SS,TPR	ESTs	12.3
	409269	AA576953	Hs.22972	SS,TM,UPF0016,SS,TM,UPF0016	hypothetical protein FLJ13352	12.0
	432596	AJ224741	Hs.278461	SS,EGF,vwa,SS,TM,vwa,	matrilin 3	11.9
35	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans,SS,TM,K_tetra,ion_t	potassium voltage-gated channel, delayed	11.9
	432912	BE007371	Hs.200313	,SS,TM,Folate_carrier	ESTs	11.9
	447033	AI357412	Hs.157601	SS	ESTs	11.8
	421155	H67879	Hs.102257	SS,Lysyl_oxidase,Aldose_epim,Epimerase,S	lysyl oxidase	11.8
40	424905	NM_002497	Hs.153704	pkinase,SS,TM,pkinase,polyprenyl_synt,	NIMA (never in mitosis gene a)-related k	11.7
	425398	AL049689	Hs.156359	SS	hypothetical protein similar to tenascin	11.6
	438167	R28363	Hs.24286	,SS,TM,7tm_1,p450,rm	ESTs	11.5
	459583	AI907673		,pkinase,	gb:IL-BT152-060399-004 BT152 Homo saplen	11.5
	423945	AA410943		death,ZU5,TM,Activin_recip,pkinase,	gb:z132h03.r1 Soares ovary tumor NbHOT H	11.4
	439820	AL360204	Hs.283953	SS	Homo sapiens mRNA full length insert cDN	11.4
45	402606			SS	NM_024826:Homo sapiens hypothetical prot	11.3
	445263	H57646	Hs.42586	,SS,Acyltransferase,	KIAA1560 protein	11.2
	430217	N47863	Hs.336901	,SS,RNA_pol_A,RNA_pol_A2,Ribosomal_S24	4e,ribosomal protein S24	11.1
	447164	AF026941	Hs.17518	,TM,IBR	Homo sapiens clg5 mRNA, partial sequence	11.1
	431385	BE178536	Hs.11090	,SS,TM	membrane-spanning 4-domains, subfamily A	11.1
50	423887	AL080207	Hs.134585	,SS,TM,BRCT,ank,ABC_tran,ABC_tran	DKFZP434G232 protein	10.9
	415385	R17798	Hs.7535	,SS,Fork_head,	COBW-like protein	10.9
	425704	U79293	Hs.159264	SS	Human clone 23948 mRNA sequence	10.7
	429859	NM_007050	Hs.225952	,SS,TM,Y_phosphatase,MAM,fn3,	protein tyrosine phosphatase, receptor t	10.4
	425523	AB007948	Hs.158244	,SS,laminin_B,laminin_EGF,laminin_Nterm	KIAA0479 protein	10.3
55	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin,SS,Peptidase	matrix metalloproteinase 3 (stromelysin	10.3
	418912	NM_000685	Hs.89472	SS,TM,7tm_1,SS,TM,7tm_1,	angiotensin receptor 1	10.3
	422026	U80736	Hs.110826	SS	trinucleotide repeat containing 9	10.3
	451952	AL120173	Hs.301663	,SS,pkinase,	ESTs	10.3
	438199	AW016531	Hs.122147	,SS,ArlGap,	ESTs	10.2
60	400608			SS,TM,SS,TM	C10001899:gl 7508633 pir T25392 hypothe	10.1
	413472	BE242870	Hs.75379	SS	solute carrier family 1 (glial high affi	10.0
	432374	W68815	Hs.301885	SS	Homo sapiens cDNA FLJ11346 fis, clone PL	9.9
	402408	NA		,SS,carb_anhydrase	NM_030920:Homo sapiens hypothetical pro	9.8
	445537	AJ245671	Hs.12844	,SS,TM,ras	EGF-like-domain, multiple 6 (EGFL6)	9.7
65	451621	AI879148	Hs.26770	SS,lipocalin,lipocalin,	fatty acid binding protein 7, brain	9.6
	405654	NA		BTB,SS	C12001521:gl 7513934 pir T31081 cca3 pr	9.6
	434988	AI418055	Hs.161160	SS	ESTs	9.6

	416220	N49776	Hs.170994	,SS,TM	hypothetical protein MGC10946	9.5
	431808	M30703	Hs.270833	SS,TM,EGF,SS	amphiregulin (schwannoma-derived growth	9.5
	414142	AW368397	Hs.150042	,SS,UDPGT	Homo sapiens cDNA FLJ14438 fis, clone HE	9.4
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of	9.4
5	418601	AA279490	Hs.86368	SS,TM,calreticulin,SS,TM,calreticulin,	calmegin	9.4
	415539	AI733681	Hs.72472	death,ZU5,TM,Activin_rec,ptkinase,	BMP-R1B	9.4
	421451	AA291377	Hs.50831	TM	ESTs	9.3
	429432	AI678059	Hs.202676	SS	synaptonemal complex protein 2	9.3
	442441	AI620662	Hs.129598	SS	ESTs	9.1
10	426429	X73114	Hs.169849	,SS,TM,in3,Ig,	myosin-binding protein C, slow-type	9.1
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin,SS,Peptidase	_matrix metalloproteinase 11 (MMP11; stro	9.1
	446693	AW004854	Hs.228320	SS	hypothetical protein FLJ23537	9.1
	419948	AB041035	Hs.93847	Ferlic_reduct,TM,Ferlic_reduct,	NM_016931:Homo sapiens NADPH oxidase 4 (	9.1
	426214	H59846	Hs.128355	SS	ESTs, Moderately similar to ALU7_HUMAN A	9.0
15	427718	AI798680	Hs.25933	,SS,TM,histone,Sec1,histone,sugar_tr	ESTs	8.9
	414812	X72755	Hs.77367	SS,IL8,SS,IL8	monokine induced by gamma interferon	8.8
	400285	NA		,TM,ABC_tran,ABC_membrane,	Eos Control	8.8
	422330	D30783	Hs.115263	SS,TM,EGF,SS,TM	epiregulin	8.8
	416182	NM_004354	Hs.79069	cyclin,SS	cyclin G2	8.8
20	420077	AW512260	Hs.87767	SS	ESTs	8.7
	452281	T93500	Hs.28792	,SS,TGF-beta,TGFb_propeptide,	Homo sapiens cDNA FLJ11041 fis, clone PL	8.7
	434531	AA642007	Hs.116369	SS	ESTs	8.6
	408380	AF123050	Hs.44532	,SS,TM,ubiquitin,7tm_3,ANF_receptor,sush	diubiquitin	8.6
	443788	AI732643	Hs.144151	TM	ESTs	8.6
25	411078	AI222020	Hs.182364	SS,SS	CococCrisp	8.5
	445495	BE622641	Hs.38489	SS,SS,ENTH,I_LWEQ,ENTH,I_LWEQ,DNA_mis_reESTs,	Weakly similar to I38022 hypotheti	8.5
	433426	H69125	Hs.133525	,SS,TM	ESTs	8.5
	424871	NM_004525	Hs.153595	SS,EGF,ldl_recept_a,ldl_recept_b,SS,TM,E	low density lipoprotein-related protein	8.4
	426215	AW963419	Hs.155223	SS	stannocalcin 2	8.4
30	409045	AA635062	Hs.50094	TM	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	8.4
	435525	AI831297	Hs.123310	TM	ESTs	8.3
	409203	AA780473	Hs.687	SS,p450,SS,p450	cytochrome P450, subfamily IVB, polypept	8.3
	424902	NM_003866	Hs.153687	SS,SS	inositol polyphosphate-4-phosphatase, ty	8.3
35	431725	X65724	Hs.2839	SS,Cys_knot,SS	Norrie disease (pseudoglioma)	8.3
	418092	R45154	Hs.106604	,death,ZU5,ptkinase,Activin_rec,	ESTs	8.3
	439840	AW449211	Hs.105445	SS	GDNF family receptor alpha 1	8.2
	427811	M81057	Hs.180884	SS,Zn_carbOpept,Propep_M14,SS,Propep_M14	carboxypeptidase B1 (tissue)	8.2
	420807	AA280627	Hs.57846	SS,cpn10	ESTs	8.2
	426320	W47595	Hs.169300	SS,TGF-beta,TGFb_propeptide,SS	transforming growth factor, beta 2	8.2
40	447078	AW885727	Hs.301570	,SS,kazal,	ESTs	8.1
	415786	AW419196	Hs.257924	SS	hypothetical protein FLJ13782	8.1
	410102	AW248508	Hs.279727	SS	Homo sapiens cDNA FLJ14035 fis, clone HE	8.0
	404347			SS	Target Exon	8.0
45	433687	AA743991		TM	gb.ny57g01.s1 NCLCGAP_P18 Homo sapiens	8.0
	421373	AA808229	Hs.167771	,SS,IMPDH_C,IMPDH_N,CBS	ESTs	8.0
	422634	NM_016010	Hs.118621	SS	CGI-82 protein	7.9
	453310	X70697	Hs.553	TM,SNF,SS,TM,SNF,	solute carrier family 6 (neurotransmitte	7.9
	435957	N39015	Hs.190368	,SS,TM	ESTs	7.8
50	407771	AL138272	Hs.62713	,TM,cpn60_TCP1,Sema,	ESTs	7.8
	443646	AI085198	Hs.164226	,TSPN,vwc,tsp_1,EGF,thiored,	ESTs	7.8
	446142	AI754693	Hs.145968	,TM,cadherin,Cadherin_C_term,	ESTs	7.7
	444649	AW207523	Hs.197628	,SS,rm,	ESTs	7.6
	435147	AL133731	Hs.4774	,TM,SDF,UPAR_LY6,	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	7.6
	439138	AI742605	Hs.193696	TM	ESTs	7.6
55	429220	AW207206	Hs.136319	SS	ESTs	7.6
	428804	AK000713	Hs.193736	,SS,UDPGT	hypothetical protein FLJ20706	7.5
	453511	AL031224	Hs.33102	SS,SS	transcription factor AP-2 beta (activat	7.5
	439809	R41396	Hs.101774	SS	hypothetical protein FLJ23045	7.5
	414869	AA157291	Hs.21479	SS	tubulin 1	7.5
60	416276	U41060	Hs.79136	SS,TM,TM	LIV-1 protein, estrogen regulated	7.5
	452862	AW378065	Hs.8687	,SS,Pep_M12B_propep,Reprolysin,tsp_1,	ESTs	7.4
	452926	AI742170	Hs.31297	,SS,TM	duodenal cytochrome b	7.4
	453331	AI240665	Hs.8895	,SS,TM,disintegrin,Pep_M12B_propep,Repro	ESTs	7.3
	420802	U22376	Hs.1334	SS,NA,myb_DNA-binding	v-myb avian myeloblastosis viral oncogen	7.3
65	450603	R43646	Hs.12422	SS	ESTs	7.2
	422867	L32137	Hs.1584	SS,EGF,tsp_3,SS,E2F_TDP,	cartilage oligomeric matrix protein (COM	7.2
	418004	U37519	Hs.87539	SS,aldech,SS,aldech,	aldehyde dehydrogenase 3 family, member	7.2

	426451	AI908165	Hs.169946	SS,GATA,	GATA-binding protein 3 (T-cell receptor	7.1
	450701	H39960	Hs.288467	,SS,LRR	Homo sapiens cDNA FLJ12280 fis, clone MA	7.1
	419519	AI198719	Hs.176376	SS	ESTs	7.1
5	410555	U92649	Hs.64311	,TM,disIntegrin,Reprolysin,	a disintegrin and metalloproteinase doma	7.1
	433138	AB029498	Hs.59729	SS,Ig,Sema,SS,Sema,efhand	semaphorin sem2	7.0
	411558	AA102670	Hs.70725	SS,TM,SS,TM	gamma-aminobutyric acid (GABA) A recepto	7.0
	409079	W87707	Hs.82065	,TM,fn3,	interleukin 6 signal transducer (gp130,	7.0
	417275	X63578	Hs.295449	SS,efhand,SS,efhand,ras	parvalbumin	7.0
	432731	R31178	Hs.287820	,SS,fn3,fn1,fn2,fn1	fibronectin 1	6.9
10	442818	AK001741	Hs.8739	WD40,SS	hypothetical protein FLJ10879	6.9
	407366	AF026942		,TM,IBR	gb:Homo sapiens c1g33 mRNA, partial sequ	6.8
	427427	AF077345	Hs.177936	SS,lectin_c,SS	ESTs	6.8
	410785	AW803341		SS	gb:IL2-UM0079-090300-050-D03 UM0079 Homo	6.7
	401045			ICE_p20,SS,ICE_p10,ICE_p20,ICE_p10,ICE_p		
15		C11001883*gi 6753278 ref NP_033938.1		c	6.7	
	418986	AI123555	Hs.81796	,SS,Reprolysin,isp_1,	ESTs	6.7
	442082	R41823	Hs.7413	,TM,EPH_1bd,pkinase,SAM,fn3,	ESTs; calyntenin-2	6.7
	442861	AA243837	Hs.57787	SS	ESTs	6.6
	418836	AI655499	Hs.161712	,TM,Activin_recp,pkinase,death,ZU5,	ESTs	6.6
20	422060	R20893	Hs.325823	,SS,TM,CD38	ESTs, Moderately similar to ALU5_HUMAN A	6.6
	444381	BE387335	Hs.283713	,SS,mito_carr	ESTs, Weakly similar to S64054 hypotheti	6.6
	404091	NA		,TM,7tm_3,ANF_receptor,	Target Exon	6.6
	417866	AW067903	Hs.82772	SS,Collagen,COLFI,TSPN,SS,TSPN	collagen, type XI, alpha 1	6.6
	428819	AL135623	Hs.193914	SS,SS	KIAA0575 gene product	6.5
25	410275	U85658	Hs.61796	,SS,Ribosomal_S4e	transcription factor AP-2 gamma (activat	6.4
	425236	AW067800	Hs.155223	SS	stannocalcin 2	6.2
	415669	NM_005025	Hs.78589	,SS,serpin,	serine (or cysteine) proteinase inhibito	6.2
	416319	AI815601	Hs.79197	SS,TM,Ig,SS,TM	CD83 antigen (activated B lymphocytes, i	6.2
	412140	AA219691	Hs.73625	,SS,kinesin,	RAB6 interacting, kinesin-like (rabkines	6.2
30	442942	AW167087	Hs.131562	,SS,Ig,Sema,pkinase,	ESTs	6.2
	446163	AA026880	Hs.25252	,SS,TM,fn3,	prolactin receptor	6.1
	443162	T49951	Hs.9029	filament,SS,filament,filament	DKFZP434G032 protein	6.1
	409802	W26713	Hs.256972	,SS,TM,DAGKa,DAGKc,	ESTs	6.1
	428479	Y00272	Hs.184572	,SS,pkinase,pkinase	cell division cycle 2, G1 to S and G2 to	6.1
35	400300	X03363		,SS,TM,pkinase,Recep_L_domain,SH2,PH,Fur	HER2 receptor tyrosine kinase (c-erb-b2,	6.1
	433404	T32982	Hs.102720	SS	ESTs	6.1
	410079	U94362	Hs.58589	Glyco_transf_8,SS	glycogenin 2	6.1
	401781			,SS,filament,Probosyltran,filament,Armad	Target Exon	6.1
	447359	NM_012093	Hs.18268	SS,adenylatekinase,	adenylate kinase 5	6.1
40	402230	NA		,SS,TM,p450,	Target Exon	6.1
	427674	NM_003528	Hs.2178	histone,SS,histone,	H2B histone family, member Q	6.1
	428398	AI249368	Hs.98558	,SS,TM	ESTs	6.0
	458098	BE550224	Hs.74170	SS	metallothionein 1E (functional)	6.0
	419968	X04430	Hs.93913	SS,IL6,IL6,	interleukin 6 (interferon, beta 2)	6.0
45	416636	N32536	Hs.42645	,SS,TM	solute carrier family 16 (monocarboxylic	6.0
	419703	AI793257	Hs.128151	,SS,zf-C2H2,	ESTs	5.8
	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin,SS,TM,Pep	matrix metalloproteinase 9 (gelatinase B	5.8
	449679	AI823951	Hs.129700	SS	tolloid-like 1	5.8
	421296	NM_002665	Hs.103253	SS	perilipin	5.8
50	442117	AW664964	Hs.128689	,SS,TM	ESTs	5.7
	400303	AA242758	Hs.79136	,SS,TM	LIV-1 protein, estrogen regulated	5.7
	419440	AB020689	Hs.90419	SS	KIAA0882 protein	5.7
	444858	AI199738	Hs.208275	SS	ESTs, Weakly similar to ALUA_HUMAN IIII	5.7
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin,SS,Peptidase	matrix metalloproteinase 13 (collagenase	5.6
55	440705	AA904244	Hs.153205	TM	ESTs	5.6
	400286	NA		SS,TM,ABC_tran,ABC_membrane,SS	C16000922:gi 7499103 pl T20903 hypothe	5.6
	446466	H38026	Hs.308	arrestin,SS	arrestin 3, retinal (X-arrestin)	5.5
	423201	NM_000163	Hs.125180	SS,TM,fn3,SS	growth hormone receptor	5.5
	433043	W57554	Hs.125019	SS	lymphoid nuclear protein (LAF-4) mRNA	5.5
60	439509	AF086332	Hs.58314	,SS,TM,Syntaxin	ESTs	5.4
	425247	NM_005940	Hs.155324	SS,Peptidase_M10,hemopexin,SS	matrix metalloproteinase 11 (MMP11; stro	5.4
	409757	NM_001898	Hs.123114	,SS,cystatin,	cystatin SN	5.4
	425292	NM_005824	Hs.155545	SS	37 kDa leucine-rich repeat (LRR) protein	5.4
	448045	AJ297436	Hs.20166	,SS,TM	prostate stem cell antigen	5.4
65	452681	AF153330	Hs.30246	,SS,TM	solute carrier family 19 (thiamine trans	5.3
	452243	AL355715	Hs.28555	SS	programmed cell death 9	5.3
	439310	AF086120	Hs.102793	,SS,TM,UDPGT,casein_kappa	ESTs	5.2

	441111	AI806867	Hs.126594	,SS,TM,Phosphodiesterase	ESTs	5.2
	452355	N54926	Hs.29202	TM,7tm_1,TM	G protein-coupled receptor 34	5.2
	427711	M31859	Hs.180408	SS	solute carrier family 25 (mitochondrial)	5.2
	418636	AW749855		,SS,TM,HECT	gb:QV4-BT0534-281299-053-c05 BT0534 Homo	5.2
5	429353	AL117406	Hs.200102	,SS,TM,ABC_tran,ABC_membrane,	ATP-binding cassette transporter MRP8	5.1
	441690	R81733	Hs.33106	,SS,HECT,zf-UBR1,PABP,14-3-3,	ESTs	5.1
	430447	W17064	Hs.332848	SS	SWI/SNF related, matrix associated, acti	5.1
	429698	AI685086	Hs.26339	,SS,ras,	ESTs, Weakly similar to S21348 probable	5.1
	425325	X52730	Hs.1892	SS,NNMT_PNMT_TEMT,SS,NNMT_PNMT_TEMT,STAR		
10				phenylethanolamine N-methyltransferase	5.1	
	423600	AI633559	Hs.310359	SS	ESTs	5.1
	414737	AI160386	Hs.125087	SS	ESTs	5.1
	403593	NA		,CIDE-N,pkinase	Target Exon	5.1
	407758	D50915	Hs.38385	SS,SS	KIAA0125 gene product	5.0
15	445234	AW137636	Hs.146059	,SS,TM	ESTs	5.0
	411165	NM_000169	Hs.69089	SS,Melibiase,BTK,PH,pkinase,SH2,SH3,Ribo	galactosidase, alpha	4.9
	420633	NM_014581	Hs.274480	SS,Iipocalln,SS,Iipocalln	odorant-binding protein 2A	4.9
	414117	W88559	Hs.1787	,TM,Ion_trans,K_tetra,	proteolipid protein 1 (Pellaeus-Merzbac	4.9
	416783	AA206186	Hs.79889	SS,TM,TM	monocyte to macrophage differentiation-a	4.9
20	401093			TM,LRRCT,TM,LRRCT,	C12000586*gi16330167 dbj BAAB6477.1  (A	4.9
	411096	U80034	Hs.68583	Peptidase_M3,	mitochondrial intermediate peptidase	4.9
	457411	AW085961	Hs.130093	SS	ESTs	4.9
	436007	AI247716	Hs.232168	,SS,adh_zinc,	ESTs	4.9
	450506	NM_004460	Hs.418	SS,DPPIV_N_term,Peptidase_S9,SS,DPPIV_N	fibroblast activation protein, alpha	4.9
25	417975	AA641835	Hs.30085	,SS,trypsin	hypothetical protein FLJ23186	4.9
	421072	AI215069	Hs.89113	SS	ESTs	4.8
	427032	AF012023	Hs.173274	,SS,14-3-3	Integrin cytoplasmic domain-associated p	4.8
	447752	M73700	Hs.105938	SS,transferrin,7tm_1,transferrin,	lactotransferrin	4.8
	403199	NA		SS,TM,Folate_carrier,SS,TM,Folate_carrie	NM_025243*Homo sapiens solute carrier f	4.8
30	427122	AW057736	Hs.323910	,SS,TM,pkinase,Recep_L_domain,SH2,PH,Fur	HER2 receptor tyrosine kinase (c-erb-b2,	4.8
	445900	AF070526	Hs.13429	,SS,Ca_channel_B,	Homo sapiens clone 24787 mRNA sequence	4.7
	413048	M93221	Hs.75182	SS,TM,lectin_c,fn2,Ricin_B_lectin,SS,TM	mannose receptor, C type 1	4.7
	419563	AA526235	Hs.193162	SS	Homo sapiens cDNA FLJ11983 fis, clone HE	4.7
	442432	BE093589	Hs.38178	SS	hypothetical protein FLJ23468	4.6
35	452093	AA447453	Hs.27860	,SS,TM,7tm_1,	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	4.6
	442323	AW016669	Hs.29190	,SS,TM,CBS,voltage_CLC	ESTs	4.6
	450606	AI668605	Hs.60380	,TM,Glyco_hydro_1	ESTs, Moderately similar to ALU5_HUMAN A	4.6
	435542	AA687376	Hs.269533	,SS,pkinase,RhoGEF,Ig,PH,SH3,	ESTs	4.6
	417576	AA339449	Hs.82285	AIRS,formyl_transf.GARS,SS,GARS,AIRS,for	phosphoribosylglycinamide formyltransfer	4.6
40	446089	AI860021	Hs.270651	,pkinase	ESTs, Moderately similar to A47582 B-cel	4.6
	445413	AA151342	Hs.12677	SS,UPF0099,SS,UPF0099,	CGI-147 protein	4.6
	424420	BE614743	Hs.146688	,SS,TM,MAPEG,	prostaglandin E synthase	4.5
	432378	AI493046	Hs.146133	,SS,TM,UDPGT	ESTs	4.5
	452190	H26735	Hs.91668	,SS,TM,PH,SH2,Furin-like,pkinase,Recep_L	Homo sapiens clone PP1498 unknown mRNA	4.5
45	434674	AA831879	Hs.135985	,SS,Hist_deacetyl,	ESTs	4.5
	419986	AI345455	Hs.78915	pkinase,OPR,	GA-binding protein transcription factor,	4.5
	421582	AI910275	Hs.1406	SS,trefol,SS,TM,Idl_recept_a,SRCR,tryps	trefol factor 1 (pS2)	4.5
	410361	BE391804	Hs.62661	SS,TM,GBP,TM,GBP	guanylate binding protein 1, interferon-	4.5
	426327	W03242	Hs.44898	SS	Homo sapiens clone TCCCTA00151 mRNA sequ	4.5
50	406639	M97711		SS,SS,Ig,	gb:Human T-cell receptor (V beta 18.1, J	4.5
	452834	AI638627	Hs.105685	,SS,DEAD,Fork_head	KIAA1688 protein	4.5
	427315	AA179949	Hs.175563	SS	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	4.4
	446733	AA853360	Hs.26040	,SS,TM,p450,	ESTs, Weakly similar to fatty acid omega	4.4
	442118	AA976718	Hs.202242	,Ig,Sema,	ESTs	4.4
55	421524	AA312082	Hs.105445	SS	GDNF family receptor alpha 1	4.4
	453060	AW294092	Hs.21594	,SS,ras,Y_phosphatase,ras	hypothetical protein MGC15754	4.4
	453403	BE466639	Hs.61779	,SS,HMG_box,filament,	Homo sapiens cDNA FLJ13591 fis, clone PL	4.4
	444301	AK000136	Hs.10760	SS,LRR,SS	asporin (LRR class 1)	4.4
	453619	H87648	Hs.33922	SS	Homo sapiens, clone MGC:9084, mRNA, comp	4.3
60	432656	NM_000246	Hs.3076	SS,LRR,	MHC class II transactivator	4.3
	426384	AI472078	Hs.303682	,SS,AirGap,	ESTs	4.3
	431701	AW935490	Hs.14658	,SS,BIR	Human chromosome 5q13.1 clone 5G8 mRNA	4.3
	416931	D45371	Hs.80485	SS,C1q,Collagen,SS,C1q,	adipose most abundant gene transcript 1	4.3
	420854	AW296927		,SS,TM,Peptidase_M1,	gb:U1-H-BW0-ajc-c-07-0-U1.s1 NCLCGAP_Su	4.3
65	418867	D31771	Hs.89404	SS,homeobox,homeobox,	msh (Drosophila) homeo box homolog 2	4.3
	443514	BE464288	Hs.141937	,SS,TM,MIP,	ESTs	4.3
	447499	AW262580	Hs.147674	,SS,TM,cadherin,cadherin	protocadherin beta 16	4.3



5	441560	F13386	Hs.7888	,pklnase,	Homo sapiens clone 23736 mRNA sequence	4.3
	409084	AA062954	Hs.141883	,SS,CUB,	ESTs	4.3
	422667	H25642	Hs.133471	,SS,TM,FMO-IIke	ESTs	4.3
	454032	W31790	Hs.194293	,SS,TM	ESTs, Weakly similar to I54374 gene NF2	4.3
	432863	AI984317	Hs.122589	TM	ESTs	4.3
	401747			,SS,filament,filament	Homo sapiens keratin 17 (KRT17)	4.3
	432882	NM_013257	Hs.279696	pklnase, pklnase_C,	serum/glucocorticoid regulated kinase-li	4.2
	437036	AI571514	Hs.133022	,SS,TM	ESTs	4.2
10	447754	AW073310	Hs.163533	,pklnase,	Homo sapiens cDNA FLJ14142 fis, clone MA	4.2
	443194	AI954968	Hs.279009	,SS,TM	matrix Gla protein	4.2
	451871	AI821005	Hs.118599	,SS,GDNF,	ESTs	4.2
	457211	AW972565	Hs.32399	WH1,WH1	ESTs, Weakly similar to S51797 vasodilat	4.2
	421566	NM_000399	Hs.1395	zf-C2H2,SS	early growth response 2 (Krox-20 (Drosop	4.2
15	431657	AI345227	Hs.105448	,SS,TM, pklnase	ESTs, Weakly similar to B34087 hypotheti	4.1
	427899	AA829286	Hs.332053	,SS,SAA_proteins,ABC_membrane,ABC_tran,	serum amyloid A1	4.1
	444779	AI192105	Hs.147170	SS	ESTs	4.1
	442295	AI827248	Hs.224398	,COLFI,vwc, Collagen,	Homo sapiens cDNA FLJ11469 fis, clone HE	4.1
	436396	AI683487	Hs.152213	,wnt,	wingless-type MMTV integration site fami	4.1
20	446039	AI150491	Hs.90756	,TM,Glyco_hydro_1	ESTs	4.1
	422938	NM_001809	Hs.1594	,SS,TM,thiolase,	centromere protein A (17kd)	4.1
	406922	S70284		SS,TM,Desaturase,SS	gb:stearoyl-CoA desaturase [human, adipo	4.1
	439285	AL133916	Hs.172572	,SS,lg, pklnase, LRRNT, LRRCT,	hypothetical protein FLJ20093	4.1
	424800	AL035588	Hs.153203	HLH,SS	MyoD family inhibitor	4.1
25	429922	Z97630	Hs.226117	,SS,TM, linker_histone, 7tm_1	H1 histone family, member 0	4.1
	447178	AW594641	Hs.192417	,SS,TM	ESTs	4.0
	409038	T97490	Hs.50002	SS,IL8,SS,IL8	small inducible cytokine subfamily A (Cy	4.0
	452747	BE153855	Hs.61460	,SS,HLH	Ig superfamily receptor LNIR	4.0
	420139	NM_005357	Hs.95351	,SS,TM,p450,	lipase, hormone-sensitive	4.0
30	408877	AA479033	Hs.130315	,SS,TM	ESTs, Weakly similar to A47582 B-cell gr	4.0
	403329	NA		SS,SS	Target Exon	4.0
	439926	AW014875	Hs.137007	SS	ESTs	4.0
	430832	AI073913	Hs.100686	SS	ESTs, Weakly similar to JE0350 Anterior	4.0
	432481	AW451545	Hs.151504	,SS, Collagen, COLFI, TSPN,	Homo sapiens cDNA FLJ11973 fis, clone HE	4.0
35	452410	AL133619	Hs.29383	,SS,TM,ras	Homo sapiens mRNA; cDNA DKFZp434E2321 (f	4.0
	418661	NM_001949	Hs.1189	SS	E2F transcription factor 3	4.0
	431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin,SS,TM,cad	cadherin 3, type 1, P-cadherin (placenta	4.0
	425071	NM_013989	Hs.154424	SS,T4_delodlnase,T4_delodlnase,	delodlnase, lodothyronine, type II	4.0
	447197	R36075		,TM,SDF,	gb:yh88b01.s1 Soares placenta Nb2HP Homo	4.0
40	428722	U76456	Hs.190787	,SS,TIMP,	tissue inhibitor of metalloproteinase 4	3.9
	428330	L22524	Hs.2256	SS,Peptidase_M10,SS,Peptidase_M10,hemopa	matrix metalloproteinase 7 (MMP7; uterin	3.9
	423242	AL039402	Hs.125783	SS	DEME-6 protein	3.9
	449048	Z45051	Hs.22920	SS,SS,TM	similar to S68401 (cattle) glucose induc	3.9
	414831	M31158	Hs.77439	,SS,cNMP_binding,Rlla,HMG_box	protein kinase, cAMP-dependent, regulato	3.9
45	413589	AW452631	Hs.313803	,SS,abhydrolase	ESTs, Highly similar to AF157833 1 noncl	3.8
	408875	NM_015434	Hs.48604	SS	DKFZP434B168 protein	3.8
	418629	BE247550	Hs.86859	SS,SH2,PH,SS,TM,PH,SH2,Furin-like, pklnas	growth factor receptor-bound protein 7	3.8
	450787	AB003190	Hs.25475	SS,TM,MIP,SS,TM,MIP,	aquaporin 7	3.8
	414870	N72264	Hs.300670	SS	KIAA1204 protein	3.8
50	450325	AI935962	Hs.26269	SS	ESTs	3.8
	407633	NM_007089	Hs.37189	TM,TM	similar to rat HREV107	3.8
	426172	AA371307	Hs.125056	,SS,DENN	ESTs	3.8
	442262	BE170651	Hs.8700	,SS,START,	deleted in liver cancer 1	3.8
	427981	AW293165	Hs.143134	SS	ESTs	3.8
55	445563	AW873608	Hs.149006	,SS,WH1,WH1	ESTs	3.8
	403943			p450,SS,p450	C5000355:gl[4503225]ref[1]NP_000765.1[ cy	3.8
	408761	AA057264	Hs.238936	,SS,TM,7tm_1,	ESTs, Weakly similar to (define not ava	3.8
	423279	AW959861	Hs.290943	SS	ESTs	3.8
	420440	NM_002407	Hs.97644	,SS,SRCR,Uteroglobin	mammaglobin 2 (MGB2; mammaglobin B; lip	3.8
60	445107	AI208121	Hs.147313	,SS,TM	ESTs, Weakly similar to I38022 hypotheti	3.7
	428303	AW974476	Hs.183601	SS,RGS,RGS,RGS	regulator of G-protein signalling 16	3.7
	411667	BE160198		TM	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.7
	427809	M26380	Hs.180878	,SS, lipase, PLAT, Sec7, PH,	lipoprotein lipase	3.7
	418203	X54942	Hs.83758	CKS,SS,CKS,	CDC28 protein kinase 2	3.7
65	430376	AW292053	Hs.12532	SS	chromosome 1 open reading frame 21	3.7
	444190	AI878918	Hs.10526	SS	cysteine and glycine-rich protein 2	3.7
	433495	AW373784	Hs.71	SS,lg,MHC_I,connexin,SCAN,SS,TM	alpha-2-glycoprotein 1, zinc	3.7
	429638	AI916662	Hs.211577	SS,TM,SS	kineclin 1 (kinesin receptor)	3.7

5	454071	AI041793	Hs.42502	,TM,7tm_1,	ESTs	3.7
	451859	H44491	Hs.252938	,SS,TM,EGF,Idl_recept_a,Idl_recept_b,EGF	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420281	AI623693	Hs.181533	,SS,AAA,	ESTs	3.7
	427691	AW194426	Hs.20726	,SS,Glycos_transf_2,	ESTs	3.7
	428824	W23624	Hs.173059	SS	ESTs	3.7
	424876	Y08585	Hs.151678	Glycos_transf_2,Ricin_B_lectin,SS,Glycos	UDP-N-acetyl-alpha-D-galactosamine;polyp	3.7
	418026	BE379727	Hs.83213	lipocalin,SS,Iipocalin,Iipocalin,ferriti	fatty acid binding protein 4, adipocyte	3.7
	457465	AW301344	Hs.122908	,SS,Pribosyltran,Sulfatase	DNA replication factor	3.7
10	417601	NM_014735	Hs.82292	PHD,pkinase,SS	KIAA0215 gene product	3.7
	407999	AI126271	Hs.49433	SS	ESTs, Weakly similar to YZ28_HUMAN HYPOT	3.7
	425548	AA890023	Hs.1905	,SS,TM,fn3,SS,TM,fn3,	prolactin receptor	3.7
	446619	AU076843	Hs.313	,SS,TM,efhand,ion_trans	secreted phosphoprotein 1 (osteopontin,	3.7
	411213	AA676939	Hs.69285	SS,TM,CUB,F5_F8_type_C,MAM,SS,TM,CUB,F5_neuropilin 1		3.6
15	406625	Y13647	Hs.119597	SS,TM,Desaturase,SS	stearoyl-CoA desaturase (delta-9-desatur	3.6
	417511	AL049176	Hs.82223	SS	chordin-like	3.6
	428769	AW207175	Hs.106771	,SS,7tm_1,SPRY,	ESTs	3.6
	407137	T97307		,SS,TM,GDA1_CD39	gbys53h05.s1 Scores fetal liver spleen	3.6
	401866			,SS,filament,	Target Exon	3.6
20	451195	U10492	Hs.438	SS,homeobox,Ets,SS,homeobox,	mesenchyme homeo box 1	3.6
	426044	AA502490	Hs.336695	SS	ESTs	3.6
	426310	NM_000909	Hs.169266	SS,TM,7tm_1,	neuropeptide Y receptor Y1	3.6
	440029	AW089705	Hs.293711	SS	ESTs, Weakly similar to S64329 probable	3.6
	408573	AA284775	Hs.43148	,SS,TM,PMP22_Claudin,	ESTs	3.6
25	431830	Y16645	Hs.271387	,SS,TM,IL8	small inducible cytokine subfamily A (Cy	3.6
	444781	NM_014400	Hs.11950	,SS,PH,lactamase_B	GPI-anchored metastasis-associated prote	3.6
	431493	AI791483	Hs.129873	,SS,p450,p450	ESTs, Weakly similar to A36036 cytochrom	3.6
	414175	AI308876	Hs.103849	,TM,hemopexin,Peptidase_M10,hemopexin,	Pehypothetical protein DKFZp761D112	3.6
	411789	AF245505	Hs.72157	lg,LRRCT,	DKFZP564I1922 protein	3.6
30	418851	AI417828	Hs.192435	,SS,TM	ESTs	3.5
	453968	AA847843	Hs.62711	,SS,HMG_box,	Homo sapiens, clone IMAGE:3351295, mRNA	3.5
	407104	S57298	Hs.323910	,SS,TM,SH2,PH,pkinase,Recep_L_domain,Fur	erb-b2 avian erythroblastic leukemia v	3.5
	449051	AW961400	Hs.333526	SS	HER2 receptor tyrosine kinase (c-erb-b2,	3.5
	434398	AA121098	Hs.3838	pkinase,POLO_box,SS,pkinase,POLO_box,	serum-inducible kinase	3.5
35	454042	H22570	Hs.172572	,SS,lg,pkinase,LRRNT,LRRCT,	hypothetical protein FLJ20093	3.5
	459496	AA08940	Hs.274450	,SS,TM,KRAB,SCAN,zf-C2H2,lg	EST	3.5
	414998	NM_002543	Hs.77729	,SS,TM	oxidised low density lipoprotein (lectin	3.5
	407756	AA116021	Hs.38260	SS,UCH-1,UCH-2,SS,TM,G_glu_transpept	ubiquitin specific protease 18	3.5
	442101	AI651930	Hs.135684	SS	ESTs	3.5
40	449722	BE280074	Hs.23960	cyclin,SS,TM,cyclin,	cyclin B1	3.5
	452554	AW452434	Hs.58006	SS	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.5
	421991	NM_014918	Hs.110488	SS	KIAA0990 protein	3.4
	420058	AK001423	Hs.94694	SS	Homo sapiens cDNA FLJ10561 fis, clone NT	3.4
	425776	U25128	Hs.159499	SS,TM,7tm_2,SS,TM,7tm_2	parathyroid hormone receptor 2	3.4
45	407846	AA426202	Hs.40403	,TM,ABC_membrane,ABC_tran,Ribosomal_S4eCbp,p300-interacting transactivator, wit		3.4
	408925	L34041	Hs.9739	,SS,TM,transport_prot,SWIB,RhoGAP,DAG_PEGlycerol-3-phosphate dehydrogenase 1 (so		3.4
	445873	AA250970	Hs.251946	,SS,rm,PABP,pkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic 1-I	3.4
	418054	NM_002318	Hs.83354	,SS,TM,mito_carr,Lysyl_oxidase	lysyl-oxidase-like 2	3.4
	414921	BE390551	Hs.77628	SS,START,SS,START,NNMT_PNMT_TEMT,	steroidogenic acute regulatory protein r	3.4
50	452268	NM_003512	Hs.28777	SS,histone,Calc_CGRP_IAPP,lg,MHC_I,SPRY,H2A histone family, member L		3.4
	428862	NM_000346	Hs.2316	SS,HMG_box,	SRY (sex determining region Y)-box 9 (ca	3.4
	412520	AA442324	Hs.795	histone,SS,histone,Bola	H2A histone family, member O	3.4
	410530	M25809	Hs.64173	ATP-synt_ab,SS,7tm_1,ATP-synt_ab	ATPase, H transporting, lysosomal (vacuo	3.4
	401780			filament,SS,filament,filament	NM_005557*Homo sapiens keratin 16 (foca	3.4
55	447131	NM_004585	Hs.17466	TM	retinoic acid receptor responder (tazaro	3.4
	418334	AA319233	Hs.5521	,SS,TM,Ribosomal_L27e,	ESTs	3.4
	415138	C18356	Hs.295944	,Kunitz_BPTI,	tissue factor pathway inhibitor 2	3.4
	421168	AF182277	Hs.330780	SS,p450,SS	cytochrome P450, subfamily IIB (phenobar	3.4
	431473	AA825686	Hs.321176	SS	ESTs, Weakly similar to S65824 reverse t	3.4
60	421379	Y15221	Hs.103982	SS,IL8,	small inducible cytokine subfamily B (Cy	3.4
	411984	NM_005419	Hs.72988	SH2,STAT,SS,STAT	signal transducer and activator of trans	3.4
	408101	AW968504	Hs.123073	,pkinase,	CDC2-related protein kinase 7	3.4
	405366			RhoGEF,PH,SS,RhoGEF,PH,	NM_003371*Homo sapiens vav 2 oncogene (	3.4
	414612	BE274552	Hs.76578	SAP,SS,FG-GAP,vwa	protein inhibitor of activated STAT3	3.4
65	411393	AW797437	Hs.69771	SS,sushi,tryptsin,vwa,rm,fibrinogen_C,fn	B-factor, properdin	3.3
	435767	H73505	Hs.117874	,SS,Peptidase_S8,P,Peptidase_S8,P	ESTs	3.3
	416403	D86961	Hs.79299	,SS,TM	lipoma HMGIC fusion partner-like 2	3.3
	433068	NM_006456	Hs.288215	,SS,Pribosyltran,	sialyltransferase	3.3

	445462	AA378776	Hs.288649	SS,SS	hypothetical protein MGC3077	3.3
	439452	AA918317	Hs.57987	SS,SS	B-cell CLL/lymphoma 11B (zinc finger pro	3.3
	452017	AF108302	Hs.27495	SS	prostate cancer associated protein 7	3.3
	409099	AK000725	Hs.50579	SS	hypothetical protein FLJ20718	3.3
5	452106	AI141031	Hs.21342	SS	ESTs	3.3
	447519	U46258	Hs.339665	SS	ESTs	3.3
	426928	AF037062	Hs.172914	,SS,adh_short,TGF-beta,TGFB_propeptide	retinol dehydrogenase 5 (11-cis and 9-ci	3.3
	438825	BE327427	Hs.79953	,SS,TM,histone,ANF_receptor,guanylate_cy	ESTs	3.3
	414575	H11257	Hs.22968	,SS,pkinase,Ig,	Homo sapiens clone IMAGE:451939, mRNA se	3.3
10	417837	AL079905	Hs.11103	SS,TGFB_propeptide,TGF-beta,SS	transforming growth factor, beta 1	3.3
	422128	AW881145		SS	gb:QV0-OT0033-010400-182-a07 OT0033 Homo	3.3
	445941	AI287371	Hs.172636	SS,SS,lipoxygenase,PLAT	ESTs	3.3
	429973	AI423317	Hs.164680	,SS,T-box,UDPGT	ESTs	3.3
	444542	AI161293	Hs.280380	SS,SS,Peptidase_M1,EGF,Ig,lectin_c,sushi	aminopeptidase	3.3
15	459561	AI547306	Hs.134981	SS	ESTs	3.3
	425741	AF052152	Hs.159412	,pkinase,	Homo sapiens clone 24628 mRNA sequence	3.3
	426501	AW043782	Hs.293616	SS	ESTs	3.3
	456508	AA502764	Hs.123469	SS	ESTs, Weakly similar to AF208855 1 BM-01	3.3
	434228	Z42047	Hs.283978	,SS,TM,7tm_1	Homo sapiens PRO2751 mRNA, complete cds	3.3
20	415752	BE314524	Hs.78776	TM	putative transmembrane protein	3.3
	400419	AF084545		,SS,Peptidase_M1,	Target	3.3
	439750	AL359053	Hs.57664	,TM,Integrin_B,Ricin_B_lectin,rm	Homo sapiens mRNA full length insert cDN	3.3
	423858	AL137326	Hs.133483	,SS,TM	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	3.3
	428514	AW236861	Hs.193139	,SS,START,NNMT,PNMT,TEM1,	ESTs	3.3
25	428698	AA852773	Hs.334838	SS	KIAA1866 protein	3.3
	446988	Y09763	Hs.22785	SS,TM,TM	gamma-aminobutyric acid (GABA) A recepto	3.3
	432072	N62937	Hs.269109	,Sema,Ig,	ESTs	3.3
	417433	BE270286	Hs.82128	SS,TM,LRRCT,LRRNT,LRR,TM,LRRCT,	5T4 oncofetal trophoblast glycoprotein	3.3
	452194	AI694413	Hs.332649	,SS,TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily	3.2
30	444051	N48373	Hs.10247	,SS,Ig,	activated leucocyte cell adhesion molecu	3.2
	420042	AW015140	Hs.161723	,SS,CUB,	ESTs	3.2
	457292	AI921270	Hs.334882	SS,TM,SS,TM,G-patch	hypothetical protein FLJ14251	3.2
	421458	NM_003654	Hs.104576	SS	carbohydrate (keratan sulfate Gal-6) sul	3.2
	431104	AW970859	Hs.313503	,Sema,Ig,	ESTs	3.2
35	443767	BE582136	Hs.9736	,SS,PCI,RasGEF,hormone_rec,zf-C4,	proteasome (prosome, macropain) 26S subu	3.2
	419589	AW973708	Hs.201925	,FGF,	Homo sapiens cDNA FLJ13446 fis, clone PL	3.2
	415447	Z97171	Hs.78454	SS,OLF,OLF,OLF,Ribosomal_L4	myoclin, trabecular meshwork inducible	3.2
	443464	BE548446	Hs.5167	SS,TM,SSF,SS,TM	Homo sapiens mRNA; cDNA DKFZp434F152 (fr	3.2
	423431	AA326062		,SS,p450,p450	gb:EST29171 Cerebellum II Homo sapiens c	3.2
40	413278	BE563085	Hs.833	,SS,TM,ubiquitin,laminin_G,laminin_EGF,k	Interferon-stimulated protein, 15 kDa	3.2
	458451	AW297181	Hs.195922	,SS,Ribosomal_L14	ESTs	3.2
	440449	AA885430	Hs.201925	,FGF,	Homo sapiens cDNA FLJ13446 fis, clone PL	3.2
	413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short,S	laminin, beta 3 (nicotin (125kD), laminin	3.2
	434876	AF160477	Hs.61460	,SS,HLH	Ig superfamily receptor LNIR	3.2
45	435575	AF213457	Hs.44234	SS,Ig,SS,TM	triggering receptor expressed on myeloid	3.2
	415773	R21651	Hs.324725	,SS,TM,Ribosomal_S3Ae,G-gamma	ESTs, Moderately similar to A47582 B-cal	3.2
	446440	AV658411	Hs.42656	SS	KIAA1681 protein	3.2
	450847	NM_003155	Hs.25590	,SS,homeobox,	stanniocalcin 1	3.2
	426075	AW513691	Hs.270149	,SS,fn3,	ESTs, Weakly similar to 2109260A B cell	3.2
50	452110	T47667	Hs.28005	,SS,TM,Activin_recp,pkinase	Homo sapiens cDNA FLJ11309 fis, clone PL	3.2
	439963	AW247529	Hs.6793	,TM,p450,Ets	platelet-activating factor acetylhydrola	3.2
	402837	NA		SS	ENSP00000241312*.DJ947L8.1.8 (novel) Sush	3.2
	439451	AF086270	Hs.278554	,SS,Chromo_shadow,chromo,	heterochromatin-like protein 1	3.1
	406654	L34041	Hs.9739	,SS,TM,transport_prot,SWI8,RhoGAP,DAG_PEG	glycerol-3-phosphate dehydrogenase 1 (so	3.1
55	417315	AI080042	Hs.336901	,SS,RNA_pol_A,RNA_pol_A2,Ribosomal_S24e,	ribosomal protein S24	3.1
	413011	AW068115	Hs.821	SS,LRR,LRRNT,SS,LRRNT,LRR,	biglycan	3.1
	414887	AA524394	Hs.294022	,SS,connexin,hormone_rec,zf-C4,connexin	hypothetical protein FLJ14950	3.1
	429197	H24471	Hs.26930	,SS,Gelsolin,	ESTs, Weakly similar to T20272 hypotheti	3.1
	448030	N30714	Hs.325960	,SS,TM	membrane-spanning 4-domains, subfamily A	3.1
60	407604	AW191962	Hs.249239	,SS,TM,C1q,	collagen, type VIII, alpha 2	3.1
	419032	J05581	Hs.89603	SS,TM,SEA,	mucin 1, transmembrane	3.1
	456672	AK002016	Hs.114727	,SS,PK,PK	Homo sapiens, clone MGC:16327, mRNA, com	3.1
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm,SS	TONDU	3.1
	452256	AK000933	Hs.28661	,TM,GDI,7tm_1,	Homo sapiens cDNA FLJ10071 fis, clone HE	3.1
65	432201	AI538613	Hs.298241	SS,TM,lypsin,SS,TM,trefol,trypsin,tref	Transmembrane protease, serine 3	3.1
	408642	AJ245210		SS	gb:Homo sapiens mRNA for immunoglobulin	3.1
	400903	NA		SS	Target Exon	3.1

	434408	AI031771	Hs.132586	,SS,Glyco_hydro_2	ESTs	3.1
	452994	AW962597	Hs.31305	SS,WD40,SS,WD40,	KIAA1547 protein	3.1
	445903	AI347487	Hs.132781	fn3,SS,TM,EF1BD	class I cytokine receptor	3.1
5	424364	AW383226	Hs.201189	SS	ESTs, Weakly similar to G01763 atrophin-	3.1
	410196	AI936442	Hs.59838	UBACT_repeat,SS,UBACT_repeat,ThiF_family	hypothetical protein FLJ10808	3.1
	419150	T29618	Hs.89640	,TM,ptkinase,fn3,	TEK tyrosine kinase, endothelial (venous	3.1
	433417	AA587773	Hs.8859	,SS,SROR,	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	418624	AI734080	Hs.104211	,Sema,lg,	ESTs	3.1
	436291	BE568452	Hs.5101	,SS,abhydrolase,	protein regulator of cytokinesis 1	3.1
10	411000	N40449	Hs.201619	SS	ESTs, Weakly similar to S33383 SEB4B pro	3.1
	412519	AA196241	Hs.73980	SS,Troponin,Hemagglutinin,SS,TM,C2,Tropo	troponin T1, skeletal, slow	3.1
	450223	AA418204	Hs.241493	,SS,pro_iscmerase,	natural killer-tumor recognition sequenc	3.1
	422790	AA809875	Hs.25933	,TM,histone,Sec1,histone,sugar_tr	ESTs	3.1
15	424269	AW137691	Hs.199754	,SS,TM,7tm_2,GPS	ESTs	3.1
	435854	AJ278120	Hs.4996	,SS,WD40	putative ankyrin-repeat containing prote	3.1
	447388	AW630534	Hs.76277	,SS,TM,rm,oxldored_q6,oxldored_q6	Homo sapiens, clone MGC:9381, mRNA, comp	3.1
	451631	R03866		SS	gb:ye79c02.s1 Scores fetal liver spleen	3.0
	448105	AW591433	Hs.298241	,SS,TM,trefoll,trypsin,trefoll	Transmembrane protease, serine 3	3.0
20	438637	BE500941	Hs.126730	,TM,PH,	ESTs, Weakly similar to KIAA1214 protein	3.0
	423024	AA593731	Hs.325823	,SS,TM,CD36	ESTs, Moderately similar to ALU5_HUMAN A	3.0
	456592	R91600		,SS,Ran_BP1,LIM,Ran_BP1,GRIP,TPR,LIM	gb:yyq10c02.r1 Scores fetal liver spleen	3.0
	425920	AI049977	Hs.162209	SS,TM,SS,TM,PMP22_Claudin,PMP22_Claudin	claudin 8	3.0
	444670	H58373	Hs.332938	,SS,TM	hypothetical protein MGC5370	3.0
	401197			arf,arf,	ENSP00000229263*HSPC213.	3.0
25	437755	AW204256	Hs.291887	,wnt,	ESTs	3.0
	452560	BE077084	Hs.336432	,SS,rm,zf-RanBP,ptkinase,C2,ptkinase_C,DA	ESTs	3.0
	410274	AA381807	Hs.61762	SS,SS	hypoxia-inducible protein 2	3.0
	450098	W27249	Hs.8109	SS	hypothetical protein FLJ21080	3.0
	404826			,SS,TM	Target Exon	3.0
30	458389	H70284	Hs.160152	,SS,RA	ESTs, Weakly similar to FPHU alpha-fetop	3.0
	408196	AL034548	Hs.43627	HMG_box,ptkinase,zf-CCHC,SS,TM,HMG_box,SRY	(sex determining region Y)-box 22	3.0
	433675	AW977653	Hs.75319	,SS,ribonuc_red_sm,	ribonucleotide reductase M2 polypeptide	3.0
	418848	AI820961	Hs.193465	,death,ZU5,ptkinase,Activin_recpt,	ESTs	3.0
35	422095	AI868872	Hs.282804	SS,Cu-oxldase,SS,Cu-oxldase,Cu-oxldase	hypothetical protein FLJ22704	3.0
	415992	C05837	Hs.145807	,SS,TM	hypothetical protein FLJ13593	3.0
	424631	AA688021	Hs.179808	SS	ESTs	3.0
	409956	AW103364	Hs.727	SS,TGF-beta,TGFb_propeptide,SS,TGF-beta,	inhibin, beta A (activin A, activin AB a	3.0
	419667	AU077005	Hs.92208	SS,disintegrin,Repolysin,Pep_M12B_prope	a disintegrin and metalloproteinase doma	3.0
	450946	AA374569	Hs.127698	SS	ESTs, Moderately similar to 2109260A B c	3.0
40	447770	AB032417	Hs.19545	Frizzled,Fz,SS,TM,Frizzled,Fz,	frizzled (Drosophila) homolog 4	3.0
	423826	U20325	Hs.1707	SS,SS	cocaine- and amphetamine-regulated trans	3.0
	418838	AW385224	Hs.35198	,SS,TM,Phosphodiect,	ectonucleotide pyrophosphatase/phosphodi	3.0
	442804	AW300118	Hs.131257	,SS,TM,G-gamma	ESTs	3.0
	432284	AA532807	Hs.105822	,SS,TM,ptkinase,	ESTs	3.0

TABLE 20A

Table 20A shows the accession numbers for those pkeys lacking unigeneID's for Table 20. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
20	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	418636	177402_1	AW749855 AA225995 AW750208 AW750206
	420854	197072_1	AW296927 AI684514 AI263168 AA261079
	422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
	423431	228162_1	AA326062 AA325758 AW982182
25	423945	233566_1	AA410943 AW948953 AA334202 AA332882
	426878	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
	433687	373061_1	AA743991 AA604852 AW272737
	447197	711623_1	R36075 AI366546 R36167
	451631	878098_1	R00866 R01523 AI806815
30	456207	165078_1	AA193450
	456592	202684_1	R91600 T87079 AA291455

TABLE 20B

Table 20B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 20. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1989) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400608	9887666	Minus	96756-97558
400903	2911732	Plus	59112-59228
401045	8117619	Plus	90044-90184,91111-91345
401093	8516137	Minus	22335-23166
401197	9719705	Plus	176341-176452
401747	9789672	Minus	118586-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401866	8018106	Plus	73126-73623
402230	9966312	Minus	29782-29932
402408	9796239	Minus	110326-110491
402578	9884928	Plus	66350-66496
402606	9909429	Minus	81747-82094
402837	9369121	Minus	2013-2186,9570-9758,11136-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320
403199	9958183	Minus	58695-59036,66618-66789
403329	8516120	Plus	96450-96598
403593	8862850	Minus	62554-62712,69449-69602
403943	7711864	Plus	100742-100904,101322-101503
404091	7684554	Minus	82121-83229
404347	9838195	Plus	74493-74829
404826	6572184	Plus	47726-48046
405366	2182280	Plus	22478-22632
405654	4895155	Minus	53624-53759

**TABLE 21: 210 GENES UP-REGULATED IN BREAST CANCER  
COMPARED TO NORMAL ADULT TISSUES THAT ARE  
LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS  
AMENABLE TO MODULATION BY SMALL MOLECULES**

Table 21 shows 210 genes up-regulated in breast cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the "average" normal adult tissue level was set to the 85<sup>th</sup> percentile value amongst 144 non-malignant tissues, and the 96<sup>th</sup> percentile value amongst 73 breast cancers was greater than or equal 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion\_transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigeneID: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of 93rd percentile tumor to 85<sup>th</sup> percentile of normal body tissue

Pkey	ExAccn	UnigeneID	Predicted Protein Domains	UnigeneTitle	R1
449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	65.7
400292	AA250737	Hs.72472	death,ZU5,TM,Activin_rec,pkinase,	BMP-R1B	55.9
424735	U31875	Hs.272499	SS,TM	short-chain alcohol dehydrogenase family	53.8
407178	AA195651	Hs.104106	SS,Dihydroorotase,	ESTs	39.3
408045	AW138959	Hs.245123	Phospholipase,Somatostatin_B,	ESTs	34.9
450375	AA009647	Hs.8850	SS,TM,disintegrin,Pep_M12B_propep,Reprol	a disintegrin and metalloproteinase doma	25.7
429170	NM_001394	Hs.2359	DSPc,Rhodanese,	dual specificity phosphatase 4	24.9
445730	AI624342	Hs.170042	SS,TM,Cation_efflux	ESTs	24.1
424634	NM_003613	Hs.151407	ig,isp_1,SS,AAA	cartilage intermediate layer protein, nu	21.7
420757	X78592	Hs.99915	hormone_rec,Androgen_recep,zf-C4,	androgen receptor (dihydrotestosterone r	21.7
424399	AI905687	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	20.3
447350	AI375572	Hs.172634	pkinase,	ESTs	19.2
456207	AA193450		SS,TM,p450,p450	gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	18.3
456938	X52509	Hs.161640	SS,TM,aminotran_1_2,Cadherin_C_term,cadhyrosine aminotransferase		18.1
402578			SS,p450,SS,TM,p450	C1001134.gil2117372 pir  65981 fatty ac	17.8
425692	D90041	Hs.155956	SS,Acetyltransf2,	N-acetyltransferase 1 (arylamine N-acety	16.7
424001	W67883	Hs.137476	pkinase,	paternally expressed 10	16.5
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10,SS,Peptidase	matrix metalloproteinase 1 (MMP1; inters	15.7
421727	Y13153	Hs.107318		kynurenine 3-monooxygenase (kynurenine 3	15.3
411869	W20027	Hs.23439	SS,Peptidase_M1,	ESTs	13.9
400289	X07820	Hs.2258	hemopexin,Peptidase_M10,SS,Peptidase_M10	matrix metalloproteinase 10 (MMP10; str	13.5
443348	AW873596	Hs.182278	SS,DENN	calmodulin 2 (phosphorylase kinase, delt	13.0
424086	AI351010	Hs.102267	SS,Lysyl_oxidase	lysyl oxidase	12.8
400295	W72838	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	12.7
408771	AW732573	Hs.47584	TM,K_tetra,ion_trans,SS,TM,K_tetra,ion_t	potassium voltage-gated channel, delayed	11.9
421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,Epimerase,S	lysyl oxidase	11.8
424905	NM_002497	Hs.153704	pkinase,SS,TM,pkinase,polyprenyl_synt,	NIMA (never in mitosis gene a)-related k	11.7
438167	R28363	Hs.24286	SS,TM,7tm_1,p450,rm	ESTs	11.5
459583	AI907673		pkinase,	gb:IL-BT152-080399-004 BT152 Homo sapien	11.5
423945	AA410943		death,ZU5,TM,Activin_rec,pkinase,	gb:zf32h03.r1 Soares ovary tumor NbHOT H	11.4
445263	H57646	Hs.42586	SS,Acyltransferase,	KIAA1560 protein	11.2

5	423887	AL080207	Hs.134585	SS,TM,BRCT,ank,ABC_tran,ABC_tran	DKFZP434G232 protein	10.9
	429859	NM_007050	Hs.225952	SS,TM,Y_phosphatase,MAM,fn3,	protein tyrosine phosphatase, receptor t	10.4
	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin,SS,Peptidase	matrix metalloproteinase 3 (stromelysin	10.3
	418912	NM_000685	Hs.89472	SS,TM,7tm_1,SS,TM,7tm_1,	angiotensin receptor 1	10.3
	451952	AL120173	Hs.301663	SS,pkinase,	ESTs	10.3
	402408	NA		SS,carb_anhydrase	NM_030920*:Homo sapiens hypothetical pro	9.8
	415539	AI733881	Hs.72472	death,ZU5,TM,Activin_rec,pkinase,	BMP-R1B	9.4
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin,SS,Peptidase	matrix metalloproteinase 11 (MMP11; stro	9.1
10	419948	AB041035	Hs.93847	Ferric_reduct,TM,Ferric_reduct,	NM_016931:Homo sapiens NADPH oxidase 4 (	9.1
	400285	NA		TM,ABC_tran,ABC_membrane,	Eos Control	8.8
	408380	AF123050	Hs.44532	SS,TM,ubiquitin,7tm_3,ANF_receptor,sushi	diubiquitin	8.6
	409203	AA780473	Hs.687	SS,p450,SS,p450	cytochrome P450, subfamily IVB, polypept	8.3
	424902	NM_003866	Hs.153687	SS,SS	inositol polyphosphate-4-phosphatase, ty	6.3
15	431725	X65724	Hs.2839	SS,Cys_knot,SS	Norrie disease (pseudoglioma)	8.3
	418092	R45154	Hs.105604	death,ZU5,pkinase,Activin_rec,	ESTs	8.3
	427811	M81057	Hs.180884	SS,Zn_carbOpept,Propep_M14,SS,Propep_M14	carboxypeptidase B1 (tissue)	8.2
	423554	M90516	Hs.1674	GATase_2,SIS,	glutamine-fructose-6-phosphate transamin	8.1
	426261	AW242243	Hs.168670	SS,TM,WD40,ubiquitin,E1-E2_ATPase,Cation	peroxisomal farnesylated protein	7.8
20	413374	NM_001034	Hs.75319	SS	ribonucleotide reductase M2 polypeptide	7.6
	432677	NM_004482	Hs.278611	SS,TM,Glycos_transf_2,Ricin_B_lectin,DPP	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.6
	456986	D38299	Hs.170917	SS,TM,7tm_1,	prostaglandin E receptor 3 (subtype EP3)	7.5
	453331	AI240665	Hs.8895	SS,TM,disIntegrin,Pep_M12B_propep,Reprol	ESTs	7.3
	407721	Y12735	Hs.38018	pkinase,	dual-specificity tyrosine-(Y)-phosphoryl	7.2
25	418004	U37519	Hs.87539	SS,aldehyd,SS,aldehyd,	aldehyde dehydrogenase 3 family, member	7.2
	410555	U92649	Hs.64311	TM,disIntegrin,Reprolysin,	a disIntegrin and metalloproteinase doma	7.1
	443695	AW204099	Hs.337720		ESTs, Weakly similar to AF126780 1 retin	6.9
	423545	AP000692	Hs.129781	GAF,PDEase	chromosome 21 open reading frame 5	6.8
	401045			ICE_p20,SS,ICE_p10,ICE_p20,ICE_p10,ICE_p		6.7
30		C11001883	*gij[8753278]ref[NP_033938.1] c			6.7
	442082	R41823	Hs.7413	TM,EPH_ld,pkinase,SAM,fn3,	ESTs; calyntenin-2	6.7
	418836	AI655499	Hs.161712	TM,Activin_rec,pkinase,death,ZU5,	ESTs	6.6
	404091	NA		TM,7tm_3,ANF_receptor,	Target Exon	6.6
	450865	AI248013	Hs.106532	zf-C2H2	ESTs, Weakly similar to I38588 reverse t	6.5
35	424085	NM_002914	Hs.139226	SS,AAA,Viral_helicase1,rm,	replication factor C (activator 1) 2 (40	6.5
	449650	AF055575	Hs.23838	TM,ion_trans,SS,TM,ion_trans,	calcium channel, voltage-dependent, L ty	6.4
	432304	AA932186	Hs.69297	TM,7tm_1,	ESTs	6.2
	415669	NM_005025	Hs.78589	SS,serpin,	serine (or cysteine) proteinase inhibito	6.2
	442942	AW167087	Hs.131562	SS,ig,Sema,pkinase,	ESTs	6.2
40	428795	R45503	Hs.97469	SS,TM	ESTs, Highly similar to A39769 N-acetyl	6.1
	428479	Y00272	Hs.184572	SS,pkinase,pkinase	cell division cycle 2, G1 to S and G2 to	6.1
	400300	X03363		SS,TM,pkinase,Recep_L_domain,SH2,PH,Furi	HER2 receptor tyrosine kinase (c-erb-b2,	6.1
	447359	NM_012093	Hs.18268	SS,adenylatekinase,	adenylate kinase 5	6.1
	402230	NA		SS,TM,p450,	Target Exon	6.1
45	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin,SS,TM,Pep	matrix metalloproteinase 9 (gelatinase B	5.8
	432328	AI572739	Hs.195471	6PF2K,PGAM,	6-phosphofructo-2-kinase/fructose-2,6-bi	5.8
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin,SS,Peptidase	matrix metalloproteinase 13 (collagenase	5.6
	400286	NA		SS,TM,ABC_tran,ABC_membrane,SS	C16000922:gij[7499103]pir[IT20903] hypothe	5.6
	425247	NM_005940	Hs.155324	SS,Peptidase_M10,hemopexin,SS	matrix metalloproteinase 11 (MMP11; stro	5.4
50	434737	AA828246	Hs.291884	UCH-1,pkinase,OPR,Rhodanese,AMP-binding,	ESTs	5.4
	439310	AF086120	Hs.102793	SS,TM,UDPGT,casein_kappa	ESTs	5.2
	441111	AI806867	Hs.126594	SS,TM,Phosphodiester,	ESTs	5.2
	452355	N54926	Hs.29202	TM,7tm_1,TM	G protein-coupled receptor 34	5.2
	427711	M31659	Hs.180408	SS	solute carrier family 25 (mitochondrial	5.2
55	429353	AL117406	Hs.200102	SS,TM,ABC_tran,ABC_membrane,	ATP-binding cassette transporter MRP8	5.1
	425325	X52730	Hs.1892	SS,NNMT_PNMT_TEMT,SS,NNMT_PNMT_TEMT,	STAR	5.1
				phenylethanolamine N-methyltransferase		5.1
	448706	AW291095	Hs.21814	SS,TM,pkinase,	interleukin 20 receptor, alpha	5.1
	403593	NA		CIDE-N,pkinase	Target Exon	5.1
60	432777	AA564991	Hs.269477	alpha-amylase,	ESTs	5.0
	446232	AI281848	Hs.194691	SS,TM,7tm_3,Ribosomal_L13	retinolic acid induced 3	4.9
	411165	NM_000169	Hs.69089	SS,Mollbiase,BTK,PH,pkinase,SH2,SH3,Ribo	galactosidase, alpha	4.9
	414117	W88559	Hs.1787	TM,ion_trans,K_tetra,	proteolipid protein 1 (Pellzaeus-Merzbac	4.9
	411096	U80034	Hs.68583	Peptidase_M3,	mitochondrial intermediate peptidase	4.9
65	450506	NM_004460	Hs.418	SS,DPPIV_N_term,Peptidase_S9,SS,DPPIV	N_fibroblast activation protein, alpha	4.9
	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	4.9
	447752	M73700	Hs.105938	SS,transferrin,7tm_1,transferrin,	lactotransferrin	4.8
	427122	AW057736	Hs.323910	SS,TM,pkinase,Recep_L_domain,SH2,PH,Furi	HER2 receptor tyrosine kinase (c-erb-b2,	4.8



	400181	NA	SS,TM,3Beta_HSD,	ENSP00000171555:CDNA FLJ10727 tis, clone	4.6
	452093	AA447453 Hs.27860	SS,TM,7tm_1,	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	4.6
	435542	AA687376 Hs.269533	SS,pkinase,RhoGEF,Ig,PH,SH3,	ESTs	4.6
	417576	AA339449 Hs.82285	AIRS,formyl_transf,GARS,SS,GARS,AIRS,for	phosphoribosylglycinamide formyltransfer	4.6
5	446089	A1860021 Hs.270651	pkinase	ESTs, Moderately similar to A47582 B-cel	4.6
	424420	BE614743 Hs.146688	SS,TM,MAPEG,	prostaglandin E synthase	4.5
	452190	H26735 Hs.91668	SS,TM,PH,SH2,Furin-like,pkinase,Recep_L_	Homo sapiens clone PP1498 unknown mRNA	4.5
	419986	A1345455 Hs.78915	pkinase,OPR,	GA-binding protein transcription factor,	4.5
	421582	A1910275 Hs.1406	SS,trefoil,SS,TM,Idl_recept_a,SRCR,tryps	trefoil factor 1 (pS2)	4.5
10	446733	AA863360 Hs.26040	SS,TM,p450,	ESTs, Weakly similar to fatty acid omega	4.4
	453060	AW294092 Hs.21594	SS,ras,Y_phosphatase,ras	hypothetical protein MGC15754	4.4
	400205	NA		NM_006265*:Homo sapiens RAD21 (S. pombe)	4.4
	420854	AW296927	SS,TM,Peptidase_M1,	gb:U1-H-BW0-ajc-c-07-0-U1.s1 NCL_CGAP_Su	4.3
	432690	AF181490 Hs.278627	SS,pyr_redox,SS,Ribosomal_L39	prenylcysteine lyase	4.3
15	441560	F13386 Hs.7888	pkinase,	Homo sapiens clone 23736 mRNA sequence	4.3
	416445	AL043004 Hs.79337	SS,pkinase,	KIAA0135 protein	4.3
	439024	R98996 Hs.35598	SS,TM,trypsin,vwd,Ig	ESTs	4.3
	432882	NM_013257Hs.279896	pkinase,pkinase_C,	serum/glucocorticoid regulated kinase-II	4.2
	447754	AW073310 Hs.163533	pkinase,	Homo sapiens cDNA FLJ14142 tis, clone MA	4.2
20	453775	NM_002916Hs.35120	SS,AAA,PI3_P14_kinase,PI3Ka,PI3K_rbd,PI3	replication factor C (activator 1) 4 (37	4.2
	431657	A1345227 Hs.105448	SS,TM,pkinase	ESTs, Weakly similar to B34087 hypotheti	4.1
	427899	AA829286 Hs.332053	SS,SAA_proteins,ABC_membrane,ABC_tran,	serum amyloid A1	4.1
	422938	NM_001809Hs.1594	SS,TM,thiolase,	centromere protein A (17kD)	4.1
	418478	U38945 Hs.1174	ank,ank	cyclin-dependent kinase inhibitor 2A (me	4.1
25	406922	S70284	SS,TM,Desaturase,SS	gb:stearoyl-CoA desaturase (human, adipo	4.1
	439285	AL133916 Hs.172572	SS,Ig,pkinase,LRRNT,LRRCT,	hypothetical protein FLJ20093	4.1
	429922	Z97630 Hs.226117	SS,TM,linker_histone,7tm_1	H1 histone family, member 0	4.1
	420139	NM_005357Hs.95351	SS,TM,p450,	lipase, hormone-sensitive	4.0
	425071	NM_013989Hs.154424	SS,T4_deiodinase,T4_deiodinase,	deiodinase, iodothyronine, type II	4.0
30	424511	BE300512 Hs.193557	SS,Y_phosphatase,Band_41	ESTs, Moderately similar to ALU7_HUMAN A	4.0
	428722	U76456 Hs.190787	SS,TIMP,	tissue inhibitor of metalloproteinase 4	3.9
	428330	L22524 Hs.2256	SS,Peptidase_M10,SS,Peptidase_M10,hemop	matrix metalloproteinase 7 (MMP7; uterin	3.9
	414831	M31158 Hs.77439	SS,cNMP_binding,R1la,HMG_box	protein kinase, cAMP-dependent, regulato	3.9
	413589	AW452631 Hs.313803	SS,abhydrolase	ESTs, Highly similar to AF157833 1 noncl	3.8
35	418629	BE247550 Hs.86859	SS,SH2,PH,SS,TM,PH,SH2,Furin-like,pkinas	growth factor receptor-bound protein 7	3.8
	413453	AA129640 Hs.128065	SS,Peptidase_C1,gpdh	ESTs	3.8
	403943		p450,SS,p450	C5000355:gil4503225[ref]NP_000765.1 cyt	3.8
	444618	AV653785 Hs.173334		ELL-RELATED RNA POLYMERASE II, ELONGATIO	3.8
	408761	AA057264 Hs.238936	SS,TM,7tm_1,	ESTs, Weakly similar to (define not ava	3.8
40	427809	M26380 Hs.180878	SS,lipase,PLAT,Sec7,PH,	lipoprotein lipase	3.7
	418203	X54942 Hs.83758	CKS,SS,CKS,	CDC28 protein kinase 2	3.7
	454071	A1041793 Hs.42502	TM,7tm_1,	ESTs	3.7
	424676	Y08565 Hs.151678	Glycos_transf_2,Ricin_B_lectin,SS,Glycos	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.7
	457465	AW301344 Hs.122908	SS,Prbbsyltran,Sulfatase	DNA replication factor	3.7
45	417601	NM_014735Hs.82292	PHD,pkinase,SS	KIAA0215 gene product	3.7
	446619	AU076643 Hs.313	SS,TM,efhand,ion_trans	secreted phosphoprotein 1 (osteopontin,	3.7
	406625	Y13647 Hs.119597	SS,TM,Desaturase,SS	stearoyl-CoA desaturase (delta-9-desatur	3.6
	428769	AW207175 Hs.106771	SS,7tm_1,SPRY,	ESTs	3.6
	426310	NM_000909Hs.169266	SS,TM,7tm_1,	neuropeptide Y receptor Y1	3.6
50	417531	NM_003157Hs.1087	SS,pkinase,vwa,Glyco_transf_8	serine/threonine kinase 2	3.6
	444781	NM_014400Hs.11950	SS,PH,lactamase_B	GPI-anchored metastasis-associated prote	3.6
	431493	A1791493 Hs.129873	SS,p450,p450	ESTs, Weakly similar to A36036 cytochrom	3.6
	428966	AF059214 Hs.194687		cholesterol 25-hydroxylase	3.6
	414175	A1308876 Hs.103849	TM,hemopexin,Peptidase_M10,hemopexin,Pep	hypothetical protein DKFZp761D112	3.6
55	455325	AW895719	TM,ion_trans,K_tetra,	gb:QV4-NN0039-290300-154-106 NN0039 Homo	3.6
	429597	NM_003816Hs.2442		a disintegrin and metalloproteinase doma	3.6
	425320	U29344 Hs.83190	Acyl_transf,adh_zinc,ketoacyl-synt,pp-bi	fatty acid synthase	3.5
	431854	AA383550 Hs.271699	IMS,SS	polymerase (DNA directed) Iota	3.5
	407104	S57296 Hs.323910	SS,TM,SH2,PH,pkinase,Recep_L_domain,Furin-erb-b2 avian erythroblastic leukemia v	HER2 receptor tyrosine kinase (c-erb-b2,	3.5
60	449051	AW961400 Hs.333526	SS	serum-inducible kinase	3.5
	434398	AA121098 Hs.3838	pkinase,POLO_box,SS,pkinase,POLO_box,	hypothetical protein FLJ20093	3.5
	454042	H22570 Hs.172572	SS,Ig,pkinase,LRRNT,LRRCT,	ubiquitin specific protease 18	3.5
	407756	AA116021 Hs.38260	SS,UCH-1,UCH-2,SS,TM,G_glu_transsept	histone deacetylase 5	3.5
	401464	AF039241 Hs.9028	Peptidase_M24,	dual specificity phosphatase 10	3.5
65	412970	AB026436 Hs.177534	DSPc,Myosin_tail,	adenylate kinase 5	3.5
	412049	N53437 Hs.18268	SS,adenylatekinase,	parathyroid hormone receptor 2	3.4
	425776	U25128 Hs.169499	SS,TM,7tm_2,SS,TM,7tm_2		

	407846	AA426202	Hs.40403	TM,ABC_membrane,ABC_tran,Ribosomal_S4eCbp/p300-interacting transactivator, wit	3.4
	406925	L34041	Hs.9739	SS,TM,transport_prot,SWIB,RhoGAP,DAG_PE-glycerol-3-phosphate dehydrogenase 1 (so	3.4
	445873	AA250970	Hs.251946	SS,rm,PABP,pkinase,14-3-3,rm	3.4
	418054	NM_002318	Hs.83354	SS,rm,mito_carr,Lysyl_oxidase	3.4
5	406815	AA833930	Hs.288036	SS,IPPT,	3.4
	410530	M25809	Hs.64173	ATP-synt_ab,SS,7tm_1,ATP-synt_ab	3.4
	407021	U52077			3.4
	421168	AF182277	Hs.330780	SS,p450,SS	3.4
	431473	AA825686	Hs.321176	SS	3.4
10	408101	AW968504	Hs.123073	pkinase,	3.4
	422083	NM_001141	Hs.111256	lipoygenase,PLAT,	3.4
	411393	AW797437	Hs.69771	SS,sushi,trypsin,vwa,rm,fibrinogen_C,fn	3.3
	435767	H73505	Hs.117874	SS,Peptidase_S8,P,Peptidase_S8,P	3.3
	433068	NM_006456	Hs.288215	SS,Pribosyltran,	3.3
15	426928	AF037062	Hs.172914	SS,adh_short,TGF-beta,TGFb_propeptide	3.3
	414575	H11257	Hs.22968	SS,pkinase,lg,	3.3
	445941	AI267371	Hs.172636	SS,SS,lipoxygenase,PLAT	3.3
	444542	AI161293	Hs.280380	SS,SS,Peptidase_M1,EGF,lg,lectin_c,sushi	3.3
	425741	AF052152	Hs.159412	pkinase,	3.3
20	434228	Z42047	Hs.283978	SS,TM,7tm_1	3.3
	433264	D85782	Hs.3229		3.3
	400419	AF084545		SS,Peptidase_M1,	3.3
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectin,rm	3.3
	417757	R19897	Hs.106604	death,ZU5,pkinase,Activin_rec,	3.3
25	452194	AI694413	Hs.332549	SS,TM,7tm_3,ANF_receptor,sushi	3.2
	421458	NM_003654	Hs.104576	SS	3.2
	443767	BE562136	Hs.9736	SS,PCI,RasGEF,hormone_rec,zf-C4,	3.2
	422648	D86983	Hs.118893	peroxidase,LRRCT,	3.2
	423431	AA326062		SS,p450,p450	3.2
30	451264	AI768235		SS,Trehalase	3.2
	452110	T47667	Hs.28005	SS,TM,Activin_rec,pkinase	3.2
	439963	AW247529	Hs.6793	TM,p450,Ets	3.2
	453941	U39817	Hs.36820	SS,DEAD,HRDC,helicase_C,	3.1
	408664	L34041	Hs.9739	SS,TM,transport_prot,SWIB,RhoGAP,DAG_PE-	3.1
35				3.1	
	453487	R31770	Hs.23540	TM,7tm_1,	3.1
	420911	U77413	Hs.100293		3.1
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm,SS	3.1
	452256	AK000933	Hs.28661	TM,GDI,7tm_1,	3.1
40	432201	AI536613	Hs.298241	SS,TM,trypsin,SS,TM,trefoil,trypsin,tref	3.1
	419150	T29618	Hs.89640	TM,pkinase,fn3,	3.1
	444443	AI149286	Hs.55099	SS	3.1
	426283	NM_003937	Hs.169139		3.1
	436291	BE568452	Hs.5101	SS,abhydrolase,	3.1
45	450223	AA418204	Hs.241493	SS,pro_isomerase,	3.1
	424269	AW137691	Hs.199754	SS,TM,7tm_2,GPS	3.1
	448105	AW591433	Hs.298241	SS,TM,trefoil,trypsin,trefoil	3.0
	452560	BE077084	Hs.336432	SS,rm,zf-RanBP,pkinase,C2,pkinase_C,DAG ESTs	3.0

## TABLE 21A

Table 21 A shows the accession numbers for those pkeys lacking unigeneID's for Table 21. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset Identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
420854	197072_1	AW296927 A1684514 A1263168 AA281079
423431	228162_1	AA326062 AA325758 AW962182
423946	233566_1	AA410943 AW948953 AA334202 AA332882
451264	863988_1	A1768235 R31400 H29082 H23107
455325	1279475_1	AW895719 N31451 N41451
456207	165078_-1	AA193450

**TABLE 21B**

**Table 21B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 21. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

**Pkey:** Unique number corresponding to an Eos probeset  
**Ref:** Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
**Strand:** Indicates DNA strand from which exons were predicted.  
**Nt\_position:** Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401045	8117619	Plus	90044-90184,91111-91345
402230	9966312	Minus	29762-29932
402408	9796239	Minus	110326-110491
402578	9884928	Plus	66350-66496
403593	6852650	Minus	62554-62712,69449-69602
403943	7711854	Plus	100742-100904,101322-101503
404091	7684554	Minus	82121-83229

**TABLE 22: 739 GENES UP-REGULATED IN BREAST CANCER  
COMPARED TO NORMAL ADULT BREAST**

Table 22 shows 739 genes up-regulated in breast cancer compared to normal adult breast. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the denominator was the 85<sup>th</sup> percentile value for 12 non-malignant breast specimens, and the 96<sup>th</sup> percentile value amongst the 73 breast cancers was greater than or equal 100 units.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigeneID: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of 90<sup>th</sup> percentile tumor to 85<sup>th</sup> percentile normal breast tissue

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
400292	AA250737	Hs.72472	BMP-R1B	51.5
424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	38.3
400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	29.9
431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	26.9
451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	25.8
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	23.2
418203	X54942	Hs.83758	CDC28 protein kinase 2	22.6
407980	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	19.8
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	18.9
445921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	18.0
409041	AB033025	Hs.50081	KIAA1199 protein	17.6
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	17.6
407824	AA147884	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HE	17.1
453160	AI263307	Hs.239884	H2B histone family, member L	17.0
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	16.1
425692	D90041	Hs.155856	N-acetyltransferase 1 (arylamine N-acety	16.1
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetl	16.0
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	15.5
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	15.1
422505	AL120862	Hs.124165	programmed cell death 9 (PDCD9)	14.9
430515	AA746503	Hs.283313	ESTs	14.7
417308	H60720	Hs.81892	KIAA0101 gene product	14.4
452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr14.4	14.2
412446	AI768015	Hs.92127	ESTs	14.2
415539	AI733881	Hs.72472	BMP-R1B	14.1
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	13.8
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	13.8
400205	NA		NM_006265*:Homo sapiens RAD21 (S. pombe)	13.5
430965	AA489732	Hs.154918	ESTs	13.4
415263	AA948033	Hs.130853	ESTs	13.3
451952	AL120173	Hs.301653	ESTs	13.2
449722	BE280074	Hs.23960	cyclin B1	13.2
406685	M18728		gb:Human nonspecific crossreacting antig	13.0
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	12.8
429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	12.8
416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	12.7
432378	AI493046	Hs.146133	ESTs	12.5
441377	BE218239	Hs.202656	ESTs	12.5
456207	AA193450		gb:zf40e07.r1 Soares_NhHMPu_S1 Homo sapi	12.4
422805	AA436989	Hs.121017	H2A histone family, member A	12.2
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	12.2
407178	AA195651	Hs.104106	ESTs	12.2

	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	12.1
	421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	12.0
	434408	AI031771	Hs.132586	ESTs	12.0
5	446591	H44186	Hs.15456	PDZ domain containing 1	11.9
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	11.8
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, delta	11.7
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	11.7
	433365	AF026944	Hs.293797	ESTs	11.6
	437836	AA156781	Hs.74170	metallothionein 1E (functional)	11.5
10	412472	AW975398	Hs.293836	ESTs	11.4
	416030	H15261	Hs.21948	ESTs	11.3
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	11.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	11.3
	411598	BE336654	Hs.70937	H3 histone family, member A	11.2
15	423600	AI633559	Hs.310359	ESTs	11.2
	430770	AA765694	Hs.123295	ESTs	11.0
	421037	AI684808	Hs.197653	programmed cell death 9 (PDCD9)	10.9
	452461	N78223	Hs.108106	transcription factor	10.7
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.6
20	417791	AW965339	Hs.111471	ESTs	10.6
	447268	AI370413	Hs.36563	hypothetical protein FLJ22418	10.4
	424001	W67883	Hs.137476	paternally expressed 10	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.4
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	10.1
25	453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	10.1
	442942	AW167087	Hs.131562	ESTs	10.1
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	10.1
	427217	AA399272	Hs.144341	ESTs	10.1
	445730	AI624342	Hs.170042	ESTs	10.0
30	432887	AI926047	Hs.162859	ESTs	10.0
	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	9.9
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	9.9
	438950	H23789	Hs.144530	EST	9.9
35	418836	AI655499	Hs.161712	ESTs	9.8
	430291	AV680345	Hs.236126	CGI-49 protein	9.8
	444665	BE613128	Hs.47783	B aggressive lymphoma gene	9.7
	407377	C16391		gb:C16391 Clontech human aorta polyA mRN	9.7
	445413	AA151342	Hs.12677	CGI-147 protein	9.7
40	443462	AI064690	Hs.171176	ESTs	9.7
	442145	AI022650	Hs.8117	erbB2-Interacting protein ERBIN	9.7
	435570	AF212222	Hs.177812	uncharacterized bone marrow protein BM04	9.7
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	9.6
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	9.6
45	449448	D60730	Hs.57471	ESTs	9.6
	433929	AI375499	Hs.27379	ESTs	9.5
	432731	R31178	Hs.287820	fibronectin 1	9.3
	411815	AA156679	Hs.125790	leucine-rich repeat-containing 2	9.3
	415385	R17798	Hs.7535	COBW-like protein	9.3
50	422026	U80736	Hs.110826	trinucleotide repeat containing 9	9.2
	432596	AJ224741	Hs.278461	matrilin 3	9.2
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	9.2
	423945	AA410943		gb:zt32h03.r1 Soares ovary tumor NbHOT H	9.1
	442432	BE093589	Hs.38178	hypothetical protein FLJ23458	9.1
55	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	9.0
	408771	AW732573	Hs.47684	potassium voltage-gated channel, delayed	9.0
	437021	AI076089	Hs.292239	ESTs	9.0
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	8.9
	428839	AI767755	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	8.9
60	402408	NA		NM_030920*:Homo sapiens hypothetical pro	8.9
	418601	AA279490	Hs.86368	calmagin	8.8
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	8.8
	419519	AI198719	Hs.176376	ESTs	8.8
	440621	AW298024	Hs.150434	ESTs	8.8
65	446142	AI754593	Hs.145968	ESTs	8.8
	418196	AI745549	Hs.26549	KIAA1708 protein	8.7
	447178	AW594641	Hs.192417	ESTs	8.7

	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	8.6
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.6
	435051	AI651474	Hs.163944	ESTs	8.6
	431374	BE258532	Hs.251871	CTP synthase	8.4
5	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	8.4
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	8.3
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	8.3
	423887	AL080207	Hs.134585	DKFZP434G232 protein	8.2
10	440941	BE268362	Hs.7535	COBW-like protein	8.2
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	8.2
	410193	AJ132592	Hs.59757	zinc finger protein 281	8.2
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	8.1
	446258	AI283476	Hs.263478	ESTs	8.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	8.1
15	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	8.1
	421650	AA781795	Hs.122587	ESTs	8.0
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	8.0
	457465	AW301344	Hs.122908	DNA replication factor	8.0
	427961	AW293165	Hs.143134	ESTs	8.0
20	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	8.0
	418216	AA682240	Hs.283099	AF15q14 protein	8.0
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	7.9
	400285	NA		Eos Control	7.9
	401464	AF039241	Hs.9028	histone deacetylase 5	7.9
25	407242	M18728		gb:Human nonspecific crossreacting antig	7.8
	422232	D43945	Hs.113274	transcription factor EC	7.8
	454024	AA893527	Hs.293907	hypothetical protein FLJ23403	7.8
	444542	AI161293	Hs.280380	aminopeptidase	7.8
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	7.7
30	437204	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	7.6
	408805	H69912	Hs.48269	vaccinia related kinase 1	7.6
	437207	T27503	Hs.15929	hypothetical protein FLJ12910	7.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	7.6
	426283	NM_003937	Hs.169139	kynureninase (L-kynureninase hydrolase)	7.5
35	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.5
	446315	NM_016293	Hs.14770	bridging integrator 2	7.5
	433428	H69125	Hs.133525	ESTs	7.5
	406639	M97711		gb:Human T-cell receptor (V beta 18.1, J	7.5
	420077	AW512260	Hs.87767	ESTs	7.4
40	457332	AA961694	Hs.105187	kinesin protein 9 gene	7.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.4
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com7.4	
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATIO7.3	
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	7.3
45	400268	NA		NM_003292:Homo sapiens translocated prom7.3	
	439509	AF086332	Hs.58314	ESTs	7.3
	407771	AL138272	Hs.62713	ESTs	7.3
	407202	N58172	Hs.109370	ESTs	7.3
	433096	AU076803	Hs.282975	carboxylesterase 2 (intestine, liver)	7.2
50	422094	AF129535	Hs.272027	F-box only protein 5	7.1
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	7.1
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE7.0	
	423739	AA398155	Hs.97600	ESTs	7.0
	448212	AI475858		gb:tc87d07.x1 NCL CGAP_CLL1 Homo sapiens7.0	
55	407277	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	7.0
	454440	BE062906	Hs.28338	KIAA1546 protein	7.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	7.0
	421373	AA808229	Hs.167771	ESTs	6.9
	431960	AW241821	Hs.301927	c6.1A	6.9
60	424704	AI263293	Hs.152086	cytochrome P450, subfamily 11J (arachido	6.8
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	6.8
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	6.8
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	6.8
	441243	AI787055	Hs.193002	ESTs	6.7
65	408380	AF123050	Hs.44532	diubiquitin	6.7
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	6.7
	446651	AA393907	Hs.97179	ESTs	6.7

	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	6.7
	437740	AA810265	Hs.122915	ESTs	6.7
	421582	AI910275	Hs.1406	trefoil factor 1 (pS2)	6.7
	427356	AW023482	Hs.97849	ESTs	6.6
5	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	422634	NM_016010	Hs.118821	CGI-62 protein	6.6
	421072	AI215059	Hs.89113	ESTs	6.5
	427718	AI798680	Hs.25933	ESTs	6.5
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	6.5
10	449343	AI151418	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.4
	409757	NM_001898	Hs.123114	cystatin SN	6.4
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	6.4
	456938	X52509	Hs.161640	tyrosine aminotransferase	6.4
	418848	AI820961	Hs.193465	ESTs	6.4
15	424902	NM_003866	Hs.153687	Inositol polyphosphate-4-phosphatase, ty	6.4
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	6.4
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.4
	407266	AI235684		gb:Homo sapiens mRNA for immunoglobulin	6.3
	411078	AI222020	Hs.182364	CocoaCrisp	6.3
20	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	6.3
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheli	6.2
	429503	AA394183	Hs.26873	ESTs	6.2
	402578			C1001134:g 2117372 p j 65981 fatty ac	6.2
25	409646	AW161391	Hs.709	deoxycytidine kinase	6.1
	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	6.1
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.1
	443709	AI082692	Hs.134662	ESTs	6.1
	420929	AI694143	Hs.296251	programmed cell death 4	6.1
30	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	6.1
	428248	AI126772	Hs.40479	ESTs	6.0
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	6.0
	453392	U23752	Hs.32964	SRX (sex determining region Y)-box 11	6.0
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.0
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	6.0
35	428585	AB007863	Hs.185140	KIAA0403 protein	6.0
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S6.0	6.0
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	6.0
	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	6.0
40	418092	R45154	Hs.106604	ESTs	6.0
	447051	AW139130	Hs.160951	ESTs, Weakly similar to Con1 [H.sapiens]	6.0
	441233	AA972965	Hs.135568	ESTs	6.0
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	6.0
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	5.9
	435525	AI831297	Hs.123310	ESTs	5.9
45	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.9
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo5.9	5.9
	422576	BE548555	Hs.118554	CGI-83 protein	5.9
	451398	AI793124	Hs.144479	ESTs	5.9
50	441881	AW968904	Hs.179566	hypothetical protein FLJ22624	5.8
	412022	AI005043	Hs.24143	Wiskott-Aldrich syndrome protein Interac	5.8
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	5.8
	447350	AI375572	Hs.172634	ESTs	5.8
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	5.8
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	5.8
55	448807	AI571940	Hs.7549	ESTs	5.8
	452281	T93500	Hs.26792	Homo sapiens cDNA FLJ11041 fls, clone PL	5.8
	421281	AI299139	Hs.17517	ESTs	5.8
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	5.8
60	400289	X07820	Hs.2258	matrix metalloproteinase 10 (MMP10; str	5.7
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	5.7
	434674	AA831879	Hs.136985	ESTs	5.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.7
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.7
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	5.7
65	438199	AW016531	Hs.122147	ESTs	5.7
	446203	Z47553	Hs.14286	flavin containing monooxygenase 5	5.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.6



	430379	AF134149	Hs.240395	potassium channel, subfamily K, member 6	5.6
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	5.6
	444756	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	5.6
5	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.6
	400301	X03635	Hs.1657	estrogen receptor 1	5.6
	447078	AW885727	Hs.301570	ESTs	5.6
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f5.5	
	438691	AA906288	Hs.212184	ESTs	5.5
10	439809	R41396	Hs.101774	hypothetical protein FLJ23045	5.5
	415766	AW419196	Hs.257924	hypothetical protein FLJ13782	5.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.5
	401645	NA		C16001440*gl 12330704 gb AAG52890.1 AF35.5	
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	5.5
15	445885	AF734009	Hs.127699	KIAA1603 protein	5.4
	439138	AF742605	Hs.193696	ESTs	5.4
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	5.4
	437536	X91221	Hs.144465	ESTs	5.4
	438167	R28363	Hs.24286	ESTs	5.4
20	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fs, clone PL	5.4
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	5.4
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.4
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	5.4
	434263	N34895	Hs.44648	ESTs	5.4
25	446382	AW205168	Hs.150823	ESTs	5.4
	422406	AF025441	Hs.116206	Opa-interacting protein 5	5.3
	438321	AA576635	Hs.6153	CGI-48 protein	5.3
	418310	AA814100	Hs.86693	ESTs	5.3
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	5.3
30	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fs, clone MA	5.3
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	5.2
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	5.2
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.2
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	5.2
35	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.2
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.2
	427427	AF077345	Hs.177936	ESTs	5.2
	403485			C3001813*gl 12737279 ref XP_012163.1  k	5.2
40	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	5.1
	421937	A1878857	Hs.109706	hemetological and neurological expressed	5.1
	426752	X69490	Hs.172004	titin	5.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	5.1
	423198	M81933	Hs.1634	cell division cycle 25A	5.1
45	412281	A1810054	Hs.14119	ESTs	5.1
	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	5.1
	453931	AL121278	Hs.25144	ESTs	5.1
	404347			Target Exon	5.1
	431806	M30703	Hs.270333	amphiregulin (schwannoma-derived growth	5.1
50	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	5.1
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.1
	450603	R43646	Hs.12422	ESTs	5.1
	434725	AK000796	Hs.4104	hypothetical protein	5.0
	435981	H74319	Hs.188620	ESTs	5.0
55	407376	AA993138	Hs.142287	ESTs, Weakly similar to ALU7_HUMAN IIII	5.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	5.0
	405348	NA		C7001634:gl 12698061 dbj BA821849.1  (AB	5.0
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fs, clone HE	5.0
	437065	AL036450	Hs.103238	ESTs	5.0
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.0
60	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.0
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.9
	403329	NA		Target Exon	4.9
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.9
	442441	A1820662	Hs.129598	ESTs	4.9
65	430375	AW371048	Hs.93758	H4 histone family, member H	4.9
	424128	AW966163		gb:EST378236 MAGI resequences, MAGI Homo	4.9
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	4.9

	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.9
	453204	R10799	Hs.191990	ESTs	4.8
5	452020	AA722012	Hs.255757	ESTs, Weakly similar to AT2A_HUMAN POTEN4.8	4.8
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.8
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	4.8
	431645	AF078849	Hs.266483	dynein light chain-A	4.8
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	4.8
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.8
10	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	4.8
	452827	AI571835	Hs.55468	ESTs	4.8
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.8
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	4.8
	419078	M93119	Hs.89584	insulinoma-associated 1	4.8
15	418973	AA233056	Hs.191518	ESTs	4.8
	447033	AI357412	Hs.157601	ESTs	4.8
	451621	AI679148	Hs.26770	fatty acid binding protein 7, brain	4.7
	419968	X04430	Hs.93913	interleukin 6 (Interferon, beta 2)	4.7
20	424326	NM_014479	Hs.145296	disintegrin protease	4.7
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.7
	429294	AA095971	Hs.198793	Homo sapiens cDNA: FLJ22463 fis, clone H	4.7
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.7
	439897	NM_015310	Hs.6763	KIAA0942 protein	4.7
	429687	AI675749	Hs.211608	nucleoporin 153kD	4.7
25	422880	AF228704	Hs.121524	glutathione reductase	4.7
	405801			NM_000390: Homo sapiens choroideremia (Ra4.6	4.6
	432435	BE218886	Hs.282070	ESTs	4.6
	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	4.6
	425354	U62027	Hs.155935	complement component 3a receptor 1	4.6
30	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	4.6
	424623	AW963062	Hs.337404	ESTs	4.6
	403366	NA		Target Exon	4.6
	402542			Target Exon	4.6
35	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	4.6
	411678	AI907114	Hs.71465	squalene epoxidase	4.6
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.6
	448072	AI459306	Hs.24908	ESTs	4.5
	408045	AW138959	Hs.245123	ESTs	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
40	447388	AW630534	Hs.76277	Homo sapiens, clone MGC:8381, mRNA, comp4.5	4.5
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	4.5
	452561	AI692181	Hs.49169	KIAA1634 protein	4.5
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo4.5	4.5
45	428801	AW277121	Hs.254881	ESTs	4.5
	428600	AI815395	Hs.184641	fatty acid desaturase 2	4.5
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.4
	437259	AI377755	Hs.120695	ESTs	4.4
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	4.4
	412863	AA121673	Hs.59757	zinc finger protein 281	4.4
50	426989	AI815206	Hs.99395	ESTs	4.4
	401866			Target Exon	4.4
	418819	AA228776	Hs.191721	ESTs	4.4
	406348			Target Exon	4.4
55	412138	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo4.4	4.4
	428550	AW297880	Hs.98661	ESTs	4.4
	411743	AW862214		gb:QV4-CT0361-301299-074-b05 CT0361 Homo4.4	4.4
	429986	BE081342	Hs.283037	HSPC039 protein	4.4
	423291	NM_004129	Hs.126590	guanylate cyclase 1, soluble, beta 2	4.4
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	4.4
60	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	4.4
	424871	NM_004525	Hs.153595	low density lipoprotein-related protein	4.3
	429575	AA706003	Hs.99387	ESTs	4.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	4.3
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.3
65	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	4.3
	437258	AL041243	Hs.174104	ESTs	4.3
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	4.3

	403011	NA	ENSP00000215330*Probable serine/threonine	4.3
	419055	AI365384	Hs.11571 Homo sapiens cDNA FLJ11570 fis, clone HE	4.3
	418661	NM_001949	Hs.1189 E2F transcription factor 3	4.3
5	407786	AA687538	Hs.38972 tetraspan 1	4.3
	429183	AB014604	Hs.197955 KIAA0704 protein	4.3
	442914	AW188551	Hs.99519 hypothetical protein FLJ14007	4.3
	441029	AI091795	Hs.179246 ESTs	4.3
	452194	AI694413	Hs.332649 olfactory receptor, family 2, subfamily	4.3
10	414821	M63635	Hs.77424 Fc fragment of IgG, high affinity Ia, re	4.2
	410102	AW248508	Hs.279727 Homo sapiens cDNA FLJ14035 fis, clone HE	4.2
	452110	T47667	Hs.28005 Homo sapiens cDNA FLJ11309 fis, clone PL	4.2
	442007	AA301116	Hs.142838 nucleolar phosphoprotein Nopp34	4.2
	417318	AW953937	Hs.12891 ESTs	4.2
15	431818	AW510444	Hs.191705 ESTs, Weakly similar to T47184 hypotheti	4.2
	443646	AI085198	Hs.164226 ESTs	4.2
	419169	AW851980	Hs.262346 ESTs, Weakly similar to S72482 hypotheti	4.2
	446839	BE091926	Hs.16244 mitotic spindle coiled-coil related prot	4.2
	423242	AL039402	Hs.125783 DEME-6 protein	4.2
20	432116	AA902953	Hs.308538 ESTs	4.2
	409038	T97490	Hs.50002 small inducible cytokine subfamily A (Cy	4.2
	445825	BE246743	Hs.288529 hypothetical protein FLJ22635	4.2
	425139	AW630488	Hs.325820 protease, serine, 23	4.2
	447387	BE247676	Hs.18442 E-1 enzyme	4.2
25	410166	AK001376	Hs.59346 hypothetical protein FLJ10514	4.1
	437295	AW779318	Hs.88417 ESTs	4.1
	430486	BE062109	Hs.241551 chloride channel, calcium activated, fam	4.1
	441790	AW294909	Hs.132208 ESTs	4.1
	410129	BE244074	Hs.58831 regulator of Fas-induced apoptosis	4.1
30	427521	AW973352	Hs.290585 ESTs	4.1
	425247	NM_005940	Hs.155324 matrix metalloproteinase 11 (MMP11; stro	4.1
	412886	AF041163	Hs.74647 Human T-cell receptor active alpha-chain	4.1
	441153	BE562826	gb:601336534F1 NIH_MGC_44 Homo sapiens c4.1	4.1
	444301	AK000136	Hs.10760 asporin (LRR class 1)	4.1
35	426711	AA383471	Hs.180669 conserved gene amplified in osteosarcoma	4.1
	405850	NA	Target Exon	4.1
	440283	AI732892	Hs.190489 ESTs	4.0
	432441	AW292425	Hs.163484 ESTs	4.0
	400284	NA	estrogen receptor 1	4.0
40	417341	N91453	Hs.102987 ESTs	4.0
	429732	U20158	Hs.2488 lymphocyte cytosolic protein 2 (SH2 doma	4.0
	411393	AW797437	Hs.69771 B-factor, properdin	4.0
	425704	U79293	Hs.159264 Human clone 23948 mRNA sequence	4.0
	419594	AA013051	Hs.91417 topoisomerase (DNA) II binding protein	4.0
45	419092	J05581	Hs.89603 mucin 1, transmembrane	4.0
	443147	AI034351	Hs.19030 ESTs	4.0
	408633	AW963372	Hs.46677 PRO2000 protein	4.0
	433404	T32982	Hs.102720 ESTs	4.0
	421506	BE302796	Hs.105097 thymidine kinase 1, soluble	4.0
50	417900	BE250127	Hs.82906 CDC20 (cell division cycle 20, S. cerevi	3.9
	414602	AW630088	Hs.76550 Homo sapiens mRNA; cDNA DKFZp564B1264 (f3.9	3.9
	413762	AW411479	Hs.848 FK506-binding protein 4 (59kD)	3.9
	404580		NM_014112*:Homo sapiens trichorhinophala	3.9
	452046	AB018345	Hs.27657 KIAA0802 protein	3.9
55	459587	AA031956	gb:zk15e04.s1 Scars_pregnant_uterus_NbH	3.9
	416658	U03272	Hs.79432 fibrillin 2 (congenital contractural ara	3.9
	426647	AA243464	Hs.294101 pre-B-cell leukemia transcription factor	3.9
	429353	AL117406	Hs.200102 ATP-binding cassette transporter MRP8	3.9
	419038	AW134924	Hs.190325 ESTs	3.9
60	418918	X07871	Hs.89476 CD2 antigen (p50), sheep red blood cell	3.9
	421977	W94197	Hs.110165 ribosomal protein L28 homolog	3.9
	442567	AI201183	Hs.130251 ESTs	3.9
	421168	AF182277	Hs.330780 cytochrome P450, subfamily IIB (phenobar	3.9
	431701	AW935480	Hs.14658 Human chromosome 5q13.1 clone 5G8 mRNA	3.9
65	418526	BE019020	Hs.85838 solute carrier family 16 (monocarboxylic	3.9
	414938	NM_002543	Hs.77729 oxidised low density lipoprotein (lectin	3.9
	422790	AA809875	Hs.25933 ESTs	3.9
	419741	NM_007019	Hs.93002 ubiquitin carrier protein E2-C	3.9

	430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	3.9
	458814	AI496957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.8
	428514	AW236861	Hs.193139	ESTs	3.8
5	434521	NM_002267	Hs.3886	karyopherin alpha 3 (Importin alpha 4)	3.8
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (Ik	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fls, clone Y7	3.8
	400021			AFFX control - HUMISGF3A/M97935_MA	3.8
10	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fls, clone PL	3.8
	445941	AI267371	Hs.172636	ESTs	3.8
	434378	AA631739	Hs.335440	EST	3.8
	429220	AW207206	Hs.136319	ESTs	3.8
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.8
15	401045			C11001883*gi 6753278 ref NP_033938.1 c	3.8
	430178	AW449612	Hs.152475	ESTs	3.8
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	3.8
	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	3.8
	436391	AJ227892	Hs.146274	ESTs	3.8
20	413011	AW068115	Hs.821	biglycan	3.8
	422121	AI767949	Hs.179833	ESTs	3.8
	452268	NM_003512	Hs.28777	H2A histone family, member L	3.8
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	3.8
	415579	AA165232	Hs.222069	ESTs	3.8
25	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.8
	427122	AW057735	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	3.7
	400286	NA		C16000922*gi 7499103 pir T20903 hypothe	3.7
	420281	AI623693	Hs.191533	ESTs	3.7
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.7
	417541	AI992191	Hs.180040	hypothetical protein FLJ22439	3.7
30	426172	AA371307	Hs.125056	ESTs	3.7
	429638	AI916662	Hs.211577	kinactin 1 (kinesin receptor)	3.7
	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	3.7
	424109	AW406578		gb:U1-HF-BL0-acg-g-06-0-U1.r1 NIH_M3C_37	3.7
35	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	3.7
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fls, clone HE	3.7
	430448	AI633553	Hs.13303	Homo sapiens cDNA: FLJ21784 fls, clone H	3.7
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	3.7
	413916	N49813	Hs.75615	apolipoprotein C-II	3.7
40	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.7
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.7
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.7
	406153			Target Exon	3.7
	445563	AW873606	Hs.149006	ESTs	3.7
45	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	3.7
	448918	AB011152	Hs.22572	KIAA0580 protein	3.7
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	3.6
	448069	U75248	Hs.20191	seven in absentia (Drosophila) homolog 2	3.6
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	3.6
50	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	3.6
	419941	X98654	Hs.93837	phosphatidylinositol transfer protein, m	3.6
	402397	AF188625	Hs.189507	phospholipase A2, group IID	3.6
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	3.6
	448106	AI800470	Hs.171941	ESTs	3.6
55	426431	NM_000458	Hs.169853	transcription factor 2, hepatic; LF-B3;	3.6
	431843	AA516420	Hs.183526	ESTs, Weakly similar to I38022 hypothe	3.6
	426878	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo3.6	3.6
	434061	AW024973	Hs.283675	NPD009 protein	3.6
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fls, clone NT	3.6
60	452101	T60298	Hs.10844	Homo sapiens cDNA FLJ14476 fls, clone MA	3.6
	427581	NM_014768	Hs.179703	KIAA0129 gene product	3.6
	409047	AW961434	Hs.31539	ESTs	3.6
	416820	NM_000402	Hs.80206	glucose-6-phosphate dehydrogenase	3.6
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fls, clone H	3.6
65	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.6
	434360	AW015415	Hs.127780	ESTs	3.6
	428970	BE276891	Hs.194691	retinoic acid induced 3	3.6
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.6

	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	3.6
	430044	AA464510	Hs.152812	ESTs	3.6
	430829	AW451999	Hs.194024	ESTs	3.6
	434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	3.6
5	439247	AF088020	Hs.46767	EST	3.6
	431542	H63010	Hs.5740	ESTs	3.5
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	3.5
	434988	AA418055	Hs.161160	ESTs	3.5
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	3.5
10	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.5
	439569	AW602166	Hs.222399	CEGP1 protein	3.5
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	3.5
	403212			NM_019595:Homo sapiens interseclin 2 (IT	3.5
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	3.5
15	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351285, mRNA	3.5
	436338	W92147	Hs.118394	ESTs	3.5
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.5
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	3.5
20	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.5
	439926	AW014875	Hs.137007	ESTs	3.5
	445873	AA250370	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	3.4
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	3.4
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	3.4
25	414921	BE390551	Hs.77628	steroidogenic acute regulatory protein r	3.4
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	3.4
	444564	AI167877	Hs.143716	ESTs	3.4
	402470	NA		Target Exon	3.4
	418120	AA213437	Hs.192249	ESTs	3.4
30	422414	AW875237	Hs.13701	ESTs	3.4
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.4
	409213	U61412	Hs.51133	PTK6 protein tyrosine kinase 6	3.4
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.4
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.4
35	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	3.4
	402359	NA		C19001991*gi12656111[gb AAK00751.1 AF23.4	3.4
	439398	AA284267	Hs.221504	ESTs	3.4
	415208	F01020	Hs.172004	tiin	3.4
	452853	AA812633	Hs.10845	ESTs	3.4
40	429345	R11141	Hs.199695	hypothetical protein	3.4
	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	3.4
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.4
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	3.4
	428977	AK001404	Hs.194698	cyclin B2	3.4
45	431611	U58766	Hs.264428	tissue specific transplantation antigen	3.4
	418286	AA622528	Hs.319825	Homo sapiens, clone IMAGE:3616574, mRNA	3.4
	436895	AF037335	Hs.5338	carbonic anhydrase XII (tumor antigen H	3.4
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.4
50	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.3
	449571	AW016812	Hs.200266	ESTs	3.3
	412777	AI335773	Hs.270123	ESTs	3.3
	420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	3.3
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.3
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	3.3
55	449065	AI627393	Hs.258998	ESTs, Weakly similar to high mobility gr	3.3
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	3.3
	430280	AA361256	Hs.237868	interleukin 7 receptor	3.3
	407777	AA161071	Hs.71465	squalene epoxidase	3.3
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit	3.3
60	414361	AI086138	Hs.204044	ESTs	3.3
	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate	3.3
	426429	X73114	Hs.169349	myosin-binding protein C, slow-type	3.3
	446163	AA026880	Hs.25252	prolactin receptor	3.3
	428566	U41763	Hs.184916	clathrin, heavy polypeptide-like 1	3.3
65	418641	BE243138	Hs.86947	a disintegrin and metalloproteinase doma	3.3
	436293	AI601188	Hs.120910	ESTs	3.3
	411257	AA628987	Hs.115274	ESTs, Highly similar to IHH_HUMAN INDIAN	3.3

	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.3
	430066	A1929659	Hs.237825	signal recognition particle 72kD	3.3
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.3
	437786	BE142681	Hs.155573	polymerase (DNA directed), eta	3.3
5	444079	H09048	Hs.23606	ESTs	3.3
	457183	H91862	Hs.118569	Dvl-binding protein IDAX (Inhibition of	3.3
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C13.3	3.3
	424563	AA446932	Hs.151428	ret finger protein 2	3.3
	450828	AW270655	Hs.193804	ESTs	3.3
10	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	3.3
	445142	AW978484	Hs.93842	Homo sapiens cDNA: FLJ22554 fis, clone H	3.3
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp58612022 (13.3	3.3
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	3.3
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	3.3
15	443247	BE614387	Hs.333893	c-Myc target JPO1	3.3
	406663	U24683	Hs.302063	immunoglobulin heavy constant mu	3.3
	434137	AA907734	Hs.124895	ESTs	3.3
	408677	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	3.3
	439101	C01765	Hs.38750	hypothetical protein FLJ11526	3.3
20	408221	AA912183	Hs.47447	ESTs	3.3
	447519	U46258	Hs.339665	ESTs	3.3
	404755	NA		Target Exon	3.3
	451871	AI821005	Hs.118599	ESTs	3.2
	420319	AW406289	Hs.96593	hypothetical protein	3.2
25	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.2
	400202	NA		NM_002795*:Homo sapiens proteasome (pro3.2	3.2
	400222	NA		NM_002082*:Homo sapiens G protein-couple	3.2
	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.2
	458098	BE550224	Hs.74170	metallothionein 1E (functional)	3.2
30	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.2
	431563	AI027643	Hs.120912	ESTs	3.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.2
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	3.2
	419703	AI793257	Hs.128151	ESTs	3.2
35	420380	AA640891	Hs.102406	ESTs	3.2
	410853	H04588	Hs.30469	ESTs	3.2
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	3.2
	432745	AI821926		gb:nf78f05.x5 NCLCGAP_Pr3 Homo sapiens	3.2
	422032	AA476986	Hs.110857	polymerase (RNA) III (DNA directed) poly	3.2
40	415339	NM_015156	Hs.78398	KIAA0071 protein	3.2
	426384	AI472078	Hs.303662	ESTs	3.2
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.2
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	3.2
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G163.2	3.2
45	434747	AA637085	Hs.220585	ESTs	3.2
	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com3.2	3.2
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	3.2
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.2
	453953	AW408337	Hs.36972	CD7 antigen (p41)	3.2
50	407758	D50915	Hs.38365	KIAA0125 gene product	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	430015	AW768399	Hs.112157	ESTs	3.2
	433313	W20128	Hs.296039	ESTs	3.2
	418334	AA319233	Hs.5521	ESTs	3.2
55	450223	AA418204	Hs.241493	natural killer-tumor recognition sequenc	3.2
	454365	AW966728	Hs.54642	methionine adenosyltransferase II, beta	3.2
	451128	AL118668		gb:DKFZp710310_r1 761 (synonym: hamy2)3.2	3.2
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	3.2
	428027	U22029	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.2
60	441197	BE244638	Hs.166	sterol regulatory element binding transc	3.2
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, au	3.2
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.2
	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	3.2
	449455	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.2
65	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	3.2
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.2
	423551	AA327598	Hs.233785	ESTs	3.2

	453553	AA036849	Hs.61829	Homo sapiens cDNA FLJ12763 fis, clone NT	3.2
	442580	AI733682	Hs.130239	ESTs	3.2
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique)	9923.2
	425700	AF076292	Hs.159251	forkhead box H1	3.2
5	417124	BE122762	Hs.25338	ESTs	3.2
	407104	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia v	3.2
	442215	AI703172	Hs.129005	ESTs, Weakly similar to 2109260A B cell	3.1
	430271	T06199	Hs.237506	DnaJ (Hsp40) homolog, subfamily B, membe	3.1
	425317	AW205118	Hs.210546	interleukin 21 receptor	3.1
10	426095	AI278023	Hs.89986	ESTs	3.1
	442313	BE388898	Hs.8215	hypothetical protein FLJ11307	3.1
	424709	AL137589	Hs.152149	hypothetical protein DKFZp434K0410	3.1
	429671	BE379335	Hs.211594	proteasome (prosome, macropain) 26S subu	3.1
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.1
15	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	3.1
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	3.1
	405017	NA		Target Exon	3.1
	433805	AA706910	Hs.112742	ESTs	3.1
	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	3.1
20	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	3.1
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.1
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypotheti	3.1
	415989	AI267700	Hs.317584	ESTs	3.1
	422907	AI879263	Hs.6986	Human glucose transporter pseudogene	3.1
25	425548	AA890023	Hs.1906	prolactin receptor	3.1
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.1
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.1
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	3.1
	458021	AI885190	Hs.156089	ESTs, Weakly similar to repressor protei	3.1
30	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.1
	400814	NA		Target Exon	3.1
	402327			Target Exon	3.1
	416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	3.1
	439838	AL355722	Hs.106875	Homo sapiens EST from clone 35214, full	3.1
35	437036	AI571514	Hs.133022	ESTs	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	3.1
	406624	AF052762		gb:Homo sapiens clone csneg8-1 immunoglo	3.1
40	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	3.1
	416379	N38857	Hs.203933	ESTs	3.1
	422823	D89974	Hs.121102	vanin 2	3.1
	433904	AI399956	Hs.208956	ESTs	3.1
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.1
45	428834	AW899713	Hs.339315	ESTs	3.1
	436043	AW953838	Hs.168630	Homo sapiens cDNA FLJ12136 fis, clone MA	3.1
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.1
	405381	NA		Target Exon	3.1
	428746	AW503820	Hs.192861	Spl-B transcription factor (Spl-1/PU.1 r	3.1
50	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f3.1	
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.1
	423305	W88562	Hs.108198	ESTs	3.1
	419123	AA234276	Hs.88253	ESTs	3.1
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serin	3.1
55	417105	X60992	Hs.81226	CD6 antigen	3.0
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.0
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	3.0
	402606			NM_024626:Homo sapiens hypothetical prot	3.0
	401451			NM_004496*:Homo sapiens hepatocyte nucle	3.0
60	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.0
	409518	BE384836	Hs.3454	KIAA1821 protein	3.0
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.0
	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.0
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.0
65	401519			C15000476*.g 12737279 ref XP_012163.1	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.0

	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	3.0
	413835	AI272727	Hs.249163	fatty acid hydroxylase	3.0
	412600	L28824	Hs.74101	spleen tyrosine kinase	3.0
5	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	3.0
	433658	L03678	Hs.156110	Immunoglobulin kappa constant	3.0
	427666	AI791495	Hs.180142	calmodulin-like skin protein	3.0
	452514	AI904898		gb:RC-BT068-130399-085 BT068 Homo sapien3.0	
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	3.0
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.0
10	437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.0
	413269	BE167525		gb:CM4-HT0509-080300-107-g07 HT0509 Homo	3.0
	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	3.0
	400929			ENSP00000252232*:Sterol regulatory eleme	3.0
15	445145	AI961702	Hs.147434	ESTs	3.0
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.0
	423279	AW959861	Hs.290943	ESTs	3.0
	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	3.0
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !III	3.0
20	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein	3.0
	413109	AW389845	Hs.110855	ESTs	3.0
	401714	NA		ENSP00000241802*:CDNA FLJ11007 FIS, CLON	3.0
	421462	AF016495	Hs.104624	aquaporin 9	3.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.0
25	453293	AA382267	Hs.10653	ESTs	3.0
	457085	AA412446	Hs.98138	ESTs	3.0
	438930	AW843633	Hs.306163	hypothetical protein AL110115	3.0



TABLE 22A

Table 22A shows the accession numbers for those pkeys lacking unigeneID's for Table 22. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407980	103087_1	AA046309 AI263500 AA046397
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
411743	1256098_1	AW862214 AW859811 AW862215
412138	1279172_1	AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
413269	1356981_1	BE167526 BE167651 BE076401 R24654
416935	163179_1	AA190712 AA190665 AA252564
422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
423945	233566_1	AA410943 AW948953 AA334202 AA332882
424109	235506_1	AW406878 AW966580 AW966151 AW966496 AA336174 AA335376 AA335537
424128	235728_1	AW966163 AA335983 AA336011 AA335668 AA335973
425331	250199_1	AW962128 AA355353 AA427363
426878	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
432745	353673_1	AI821926 AA658826 AA564492 AA635129 AI791191
441153	51084_2	BE562826 BE378727
448212	755099_1	AI475858 AW969013
451128	859865_1	AL118668 D78823 AI762176
452514	920172_1	AI904898 AI904849 AI904899
456207	165078_1	AA193450

**TABLE 22B**

**Table 22B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 22. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	400814	8569925	Minus	72840-72924,74761-74849
	400929	7651921	Minus	122033-122241,123483-124028
20	401045	8117619	Plus	90044-90184,91111-91345
	401451	6634068	Minus	119926-121272
	401519	6649315	Plus	157315-157950
	401645	7657839	Minus	34986-35133
	401714	6715702	Plus	96484-96681
25	401866	8018106	Plus	73126-73623
	402327	7656695	Minus	108675-108770,109801-109910
	402359	9211204	Minus	40403-41961
	402408	9796239	Minus	110326-110491
	402470	9797107	Plus	195129-195776
30	402542	9801558	Minus	67076-67594
	402578	9884028	Plus	66350-66496
	402606	9909429	Minus	81747-82094
	403011	6693597	Minus	3468-3623
	403212	7630897	Minus	156037-156210
35	403329	8516120	Plus	96450-96598
	403356	8783692	Minus	49323-49652
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	404347	9838195	Plus	74493-74829
	404580	6539738	Minus	240588-241589
40	404755	7706327	Minus	53729-53846
	405017	6532084	Plus	35551-35690
	405348	2914717	Minus	43310-43462
	405381	6006920	Minus	7636-8054
	405801	2924321	Plus	63469-63694
45	405850	6164995	Plus	13871-14110
	406153	9929734	Minus	12902-13069
	406348	9255985	Minus	71754-71944

**TABLE 23: 320 GENES DOWN-REGULATED IN BREAST CANCER  
COMPARED TO NORMAL ADULT BREAST**

- 5 **Table 23** shows 320 genes down-regulated in breast cancer compared to normal adult breast. These were selected as for Table 22, except that the numerator was set to the median value for 12 non-malignant breast specimens, the denominator was set to the median value amongst the 73 breast cancers, the 90<sup>th</sup> percentile value amongst the 12 non-malignant breast specimens was greater than or equal 80 units, and the ratio was greater than or equal to 4.0 (i.e. 4-fold down-regulated in tumor vs. normal breast).
- 10

15 Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigeneID: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of 50<sup>th</sup> percentile normal body tissue to 75<sup>th</sup> percentile tumor

20	Pkey	ExAccn	UnigeneID	UnigeneTitle	Ratio
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	22.4
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	17.4
	445263	H57646	Hs.42566	KIAA1560 protein	15.4
25	418935	T28489	Hs.89485	carbonic anhydrase IV	15.0
	407228	M25079	Hs.155376	hemoglobin, beta	14.6
	417511	AL049176	Hs.82223	chordin-like	14.6
	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	14.3
	412442	A1983730	Hs.26530	serum deprivation response (phosphatidyl	13.6
30	410544	A1446543	Hs.95511	ESTs	12.6
	412047	AA934589	Hs.49696	ESTs	12.2
	422667	H25642	Hs.133471	ESTs	12.0
	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	12.0
	423201	NM_000163	Hs.125180	growth hormone receptor	11.7
35	422163	AF027208	Hs.112360	prominin (mouse)-like 1	10.8
	428769	AW207175	Hs.106771	ESTs	10.6
	407049	X72632		NM_021724*:Homo sapiens nuclear receptor	10.1
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	9.8
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	9.8
40	406791	AI220584	Hs.272572	hemoglobin, alpha 2	9.5
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	9.5
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	9.4
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.0
	411939	AI365585	Hs.146246	ESTs	9.0
45	410532	T53088	Hs.155376	hemoglobin, beta	8.9
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.8
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	8.7
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	8.6
	435265	AA779958	Hs.185932	ESTs	8.5
50	422511	AI076442	Hs.117938	collagen, type XVII, alpha 1	8.4
	433138	AB029496	Hs.59729	semaphorin sem2	8.3
	402195			NM_004497*:Homo sapiens hepatocyte nucle	8.1
	429350	AI754634	Hs.131987	ESTs	8.1
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheil	8.1
55	406643	N77976	Hs.272572	hemoglobin, alpha 2	8.0
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fls, clone H	8.0
	417225	AA815048	Hs.24078	hypothetical protein FLJ12649	7.8
	437569	AA760849	Hs.294052	ESTs	7.5
	436062	AK000027	Hs.98633	ESTs	7.5
60	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	7.5
	430327	AW973636	Hs.55931	ESTs	7.4

5	447577	AI393693	Hs.183297	DKFZP566F2124 protein	7.4
	446039	AI150491	Hs.90756	ESTs	7.2
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	7.2
	424455	AA452006	Hs.333199	ESTs	7.1
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	7.1
10	442792	AI352340	Hs.131194	ESTs	7.0
	406714	AI219304	Hs.283108	hemoglobin, gamma G	6.9
	407571	AI446183	Hs.9572	ESTs, Highly similar to CYA5_HUMAN ADENY	6.8
	429580	AA346839	Hs.209100	DKFZP434C171 protein	6.7
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	6.7
15	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	6.7
	420205	AA256395	Hs.88156	ESTs	6.6
	404368	NA		ENSP00000241075*TRRAP PROTEIN.	6.6
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	6.5
	417090	AA193282	Hs.85863	ESTs, Weakly similar to B34612 zinc fing	6.5
20	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	6.5
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	6.5
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	6.4
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	6.4
	416253	BE250659	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA	6.4
25	435885	AA701483	Hs.36341	ESTs	6.3
	402779	NA		Target Exon	6.3
	418138	AA213626	Hs.136204	EST	6.3
	439335	AA742697	Hs.62492	ESTs, Weakly similar to B39066 proline-r	6.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	6.2
30	411478	BE143068		gb:MR0-HT0158-030200-003-b09 HT0158 Homo	6.2
	452654	BE004783		gb:MR2-BN0114-270400-004-e11 BN0114 Homo	6.1
	447359	NM_012093	Hs.18268	adenylate kinase 5	6.1
	414323	NM_014759	Hs.334688	KIAA0273 gene product	6.1
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	6.1
35	417011	F08212	Hs.234898	ESTs, Weakly similar to 2109260A B cell	6.0
	400089	NA		Eos Control	6.0
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	5.9
	440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS [H	5.9
	454404	BE067414		gb:MR4-BT0355-200100-201-e05 BT0355 Homo	5.9
40	436704	AA062610	Hs.148050	EST	5.9
	406563	NA		Target Exon	5.9
	433490	AW451023	Hs.65848	hypothetical protein DKFZp7610132	5.9
	419313	AA843387	Hs.87279	ESTs	5.9
	409196	NM_001874	Hs.334873	carboxypeptidase M	5.8
45	410882	AW809163		gb:MR4-ST0116-261099-012-a03 ST0116 Homo	5.8
	453469	AB014533	Hs.33010	KIAA0633 protein	5.8
	441899	AI372588	Hs.8022	TU3A protein	5.8
	426210	AA372052	Hs.334559	Homo sapiens cDNA FLJ14458 fis, clone HE	5.8
	413065	BE063555		gb:CM1-BT0283-081199-033-d09 BT0283 Homo	5.8
50	454192	AW876813	Hs.3343	phosphoglycerate dehydrogenase	5.7
	425187	AW014486	Hs.22509	ESTs	5.7
	429757	AW452355	Hs.256037	ESTs	5.7
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	5.7
	416284	AI695473	Hs.298006	ESTs	5.7
55	428553	AA181641	Hs.184907	G protein-coupled receptor 1	5.6
	404689	NA		Target Exon	5.6
	438887	R68857	Hs.265499	ESTs	5.6
	408082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	5.6
	449748	H23963	Hs.32043	ESTs	5.6
60	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	5.5
	452205	C15819		gb:C15819 Clontech human aorta polyA mRNA	5.5
	434040	AW444613	Hs.288809	hypothetical protein FLJ20159	5.5
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	5.5
	450606	AI668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	5.5
65	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	5.5
	401635			C11000703:gil10048448[ref NP_C65258.1 ] g	5.5
	435107	T99079	Hs.191194	ESTs	5.5
	444432	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145kD	5.5
	434715	BE005346	Hs.116410	ESTs	5.5
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	5.5
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	5.5

5	454016	AW016806	Hs.233108	ESTs	5.5
	414913	R25621		gb:yh45f06.r1 Soares placenta Nb2HP Homo	5.4
	458033	AA017590	Hs.129907	ESTs	5.4
	441003	BE172240	Hs.126379	ESTs, Weakly similar to I38022 hypotheti	5.4
	450637	N49826	Hs.18602	ESTs	5.4
10	442398	AA994520		gb:ou42g09.s1 Soares_NFL_T_GBC_S1 Homo s	5.4
	403612	NA		Target Exon	5.3
	407102	AA007629	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	5.3
	410057	R66634	Hs.268107	multimerin	5.3
	428232	BE272452	Hs.183109	monoamine oxidase A	5.3
15	432769	AA620814	Hs.144959	ESTs	5.3
	431344	R99530	Hs.272572	hemoglobin, alpha 2	5.3
	427032	AF012023	Hs.173274	integrin cytoplasmic domain-associated p	5.3
	406305	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	5.3
	437411	AW613948	Hs.194915	ESTs	5.3
20	442800	AI809481	Hs.131227	ESTs	5.3
	402054	NA		Target Exon	5.3
	432085	AF212829	Hs.272406	potassium channel, subfamily K, member 9	5.3
	415313	R59638	Hs.6181	ESTs	5.2
	459159	AI904646		gb:QV-BT065-020399-103 BT065 Homo sapien	5.2
25	427164	AB037721	Hs.173871	KIAA1300 protein	5.2
	441391	BE467930	Hs.170381	ESTs	5.2
	458959	AI285901	Hs.181297	ESTs	5.2
	402698	NA		ENSP00000251335*:DJ1003J2.1 (sodium and	5.2
	401810	NA		Target Exon	5.2
30	438879	AA827674	Hs.189073	ESTs	5.2
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.2
	427809	M26380	Hs.180878	lipoprotein lipase	5.1
	456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	5.1
	451186	AW023469	Hs.65256	ESTs, Weakly similar to leucine-rich gli	5.1
35	451882	AI821324	Hs.100445	ESTs	5.1
	402583	NA		NM_021620:Homo sapiens PR domain contain	5.1
	431130	NM_006103	Hs.2719	HE4; WFDG2; putative ovarian carcinoma m	5.1
	458218	AI435179	Hs.126820	ESTs	5.1
	416083	R53467	Hs.269122	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
40	455282	BE143867		gb:MR0-HT0164-070100-013-h02 HT0164 Homo	5.1
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	5.1
	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guanylate	5.1
	407891	AA486620	Hs.41135	endomucin-2	5.0
	408610	AW026692	Hs.224829	ESTs	5.0
45	445967	D59597	Hs.118821	CGI-62 protein	5.0
	434813	AI524307	Hs.182870	ESTs	5.0
	437526	AI076012	Hs.121388	ESTs, Weakly similar to MDHC_HUMAN MALAT	5.0
	454775	BE160229		gb:QV1-HT0413-090200-062-a12 HT0413 Homo	5.0
	409451	AF012626	Hs.54472	fragile X mental retardation 2	5.0
50	409853	AW502327		gb:U1-HF-BR0p-aka-a-07-0-U1.r1 NIH_MGC_5	5.0
	405062			Target Exon	5.0
	446490	AK000706	Hs.15125	hypothetical protein FLJ20699	5.0
	417622	AW298163	Hs.82318	WAS protein family, member 3	5.0
	421978	AJ243662	Hs.110196	NICE-1 protein	5.0
55	440338	R62431	Hs.12758	ESTs	5.0
	415421	R35009	Hs.24903	ESTs	5.0
	417574	R00348		gb:ye69e06.r1 Soares fetal liver spleen	5.0
	408882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7	5.0
	447998	AI768289	Hs.304389	ESTs	4.9
60	445613	BE550889	Hs.158491	ESTs	4.9
	443074	AW341470	Hs.144907	ESTs	4.9
	451324	AI783600	Hs.208052	ESTs	4.9
	432433	AW014734	Hs.157969	ESTs	4.9
	449654	AI989812	Hs.199850	ESTs	4.9
65	414519	N94587	Hs.55063	ESTs	4.9
	457531	AW973716	Hs.13913	KIAA1577 protein	4.9
	433200	AA682722	Hs.192725	ESTs	4.9
	430782	AF026263	Hs.247920	cholinergic receptor, muscarinic 5	4.8
	427555	AW137094	Hs.97990	ESTs	4.8
	433545	AA868510	Hs.112496	ESTs	4.8
	420334	AI349351	Hs.118944	hypothetical protein FLJ22477	4.8

	421795	X63094	Hs.283822	Rhesus blood group, D antigen	4.8
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	4.8
	413072	BE063965		gb:QV3-BT0296-140200-085-h01 BT0296 Homo	4.8
5	443721	AW450451	Hs.266355	ESTs	4.8
	408053	AW139474	Hs.246862	ESTs	4.8
	427067	AA843716	Hs.177927	ESTs	4.7
	442969	AI025499	Hs.132238	ESTs	4.7
	426220	AI383475	Hs.171697	ESTs, Weakly similar to T13924 sdk prote	4.7
	414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo sapiens c	4.7
10	426893	AA398716	Hs.97418	ESTs	4.7
	434046	AW292618	Hs.113011	ESTs	4.7
	401590	NA		Target Exon	4.7
	457971	AW134679	Hs.242849	ESTs	4.7
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	4.6
15	443793	AA045290	Hs.25930	ESTs, Weakly similar to 2109260A B cell	4.6
	407737	R49187	Hs.6659	ESTs	4.6
	441955	AA972327	Hs.142903	ESTs	4.6
	441499	AW298235	Hs.101689	ESTs	4.6
	447517	AI382726	Hs.182434	ESTs	4.6
20	403017			Target Exon	4.5
	450580	N40087	Hs.15248	ESTs	4.5
	404611	H58589	Hs.35155	Homo sapiens cDNA FLJ11027 fis, clone PL	4.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regula	4.5
	459290	NM_001545	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.5
25	444341	AI142027	Hs.146650	ESTs	4.5
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	4.5
	449638	AW204277	Hs.250723	hypothetical protein MGC2747	4.5
	434418	AF134707	Hs.278679	a disintegrin and metalloproteinase doma	4.5
	447360	AI375984	Hs.167216	ESTs	4.5
30	419583	F00312		gb:HSBB0D101 STRATAGENE Human skeletal m	4.5
	440698	AI348455	Hs.147492	Homo sapiens cDNA FLJ11777 fis, clone HE	4.5
	451199	AI290653	Hs.124758	ESTs	4.5
	438338	NM_014861	Hs.6168	KIAA0703 gene product	4.5
35	433756	AW015933	Hs.112654	Homo sapiens, clone MGC:9764, mRNA, comp	4.5
	423301	S67580	Hs.1645	cytochrome P450, subfamily IVA, polypept	4.5
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	4.5
	439745	AL389981	Hs.149219	Homo sapiens mRNA full length insert cDN	4.5
	424137	AA335769	Hs.16262	ESTs	4.5
	449338	H73444	Hs.394	adrenomedullin	4.5
40	434744	N94635	Hs.283828	Homo sapiens genomic DNA, chromosome 21q	4.5
	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	4.5
	443510	NM_012190	Hs.9520	formyltetrahydrofolate dehydrogenase	4.5
	415754	AA169114	Hs.12247	hypothetical protein FLJ11413	4.5
	415986	Z43619		gb:HSC1GE121 normalized Infant brain cDN	4.5
45	457416	BE142052	Hs.62654	kringle-containing transmembrane protein	4.5
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	4.4
	437120	AI356125	Hs.157767	ESTs, Weakly similar to HXA2_HUMAN HOMEO	4.4
	453950	AA156998	Hs.211588	eukaryotic translation Initiation factor	4.4
	401093			C12000586*:g j6330167 dbj BAA86477.1  {A	4.4
50	436935	AW206494	Hs.253580	ESTs	4.4
	457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	4.4
	428222	AL133112	Hs.183085	Homo sapiens mRNA; cDNA DKFZp434K098 (fr	4.4
	442705	AI264634	Hs.131127	ESTs	4.4
	437409	AL359599	Hs.283850	Homo sapiens mRNA; cDNA DKFZp547C126 (fr	4.4
55	458494	AI380906	Hs.158436	ESTs	4.4
	410490	H03589		gb:y 42d08.r1 Soares placenta Nb2HP Homo	4.4
	416069	R37101	Hs.20982	ESTs	4.4
	438463	AA807958	Hs.314232	ESTs	4.4
	444043	AI499723	Hs.135089	ESTs	4.4
60	438327	H87407	Hs.172944	chorionic gonadotropin, beta polypeptide	4.4
	457711	AF147401	Hs.23917	ESTs	4.3
	400870			C11000905:g j11692565 gb AAG39879.1 AF28	4.3
	441425	AA933590	Hs.28937	homeobox protein from AL590526	4.3
	416267	H45384		gb:yn99c10.r1 Soares adult brain N2b5HB5	4.3
65	407262	M12873		gb:Human Ig rearranged H-chain mRNA VDJ4	4.3
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26886 hypotheti	4.3
	403263	NA		Target Exon	4.3

	410034	BE067414		gb:MR4-BT0355-200100-201-e05 BT0355 Homo	4.3
	456804	AI421645	Hs.139651	caveolin 2	4.3
	448427	BE395260	Hs.309438	EST	4.3
	416831	D45371	Hs.80485	adipose most abundant gene transcript 1	4.3
5	421296	NM_002666	Hs.103253	perilipin	4.3
	400973	NA		ENSP00000236657*:Mucin 5B (Fragment).	4.3
	452602	AW368194	Hs.55962	ESTs	4.3
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	4.3
	405016			CY000171*:gil9280405 gb AAF86402.1 AF245	4.3
10	435104	AI475671	Hs.88607	ESTs, Highly similar to F-box protein FB	4.3
	406118			ENSP00000246632:CDNA FLJ20261 fis, clone	4.3
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo s	4.3
	429745	AA480818	Hs.221736	ESTs	4.3
	433088	AW451206	Hs.115899	ESTs	4.3
15	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	4.3
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	4.3
	447384	AI377221	Hs.40528	ESTs	4.2
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	4.2
	444975	AV652165	Hs.182482	ESTs, Weakly similar to T00362 hypotheti	4.2
20	403921	NA		C5000212*:gil10047237 dbj BAB13407.1  (A	4.2
	451477	AI798425	Hs.42710	ESTs	4.2
	406344			C5001660:gil11611537 dbj BAB18935.1  (AB	4.2
	416970	AA191201	Hs.35861	DKFZP586E1621 protein	4.2
	413662	BE155866	Hs.25522	KIAA1808 protein	4.2
25	458504	AW070634	Hs.144794	ESTs	4.2
	404682	NA		C9001188*:gil12738842 ref NP_073725.1  p	4.2
	418089	N69913	Hs.6858	ESTs, Weakly similar to I78885 serine/th	4.2
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	4.2
	446532	AW975460	Hs.143563	ESTs	4.2
30	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	4.2
	418425	AI871247	Hs.6262	hypothetical protein MGC8407	4.2
	419589	AW873708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	4.2
	457029	AA397789	Hs.161803	ESTs	4.2
	447880	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	4.2
35	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	4.2
	440610	AI733098	Hs.130800	ESTs	4.2
	439590	AF086410		gb:Homo sapiens full length insert cDNA	4.2
	427240	AA399975	Hs.274151	ligatin	4.2
	408932	AW594172	Hs.278513	TP53TG3 protein	4.2
40	436112	T77545	Hs.187559	ESTs	4.2
	444382	AI144152	Hs.58246	ESTs	4.2
	456716	AA318060	Hs.135121	hypothetical protein FLJ22415	4.2
	419846	NM_015977	Hs.285681	Williams-Beuren syndrome chromosome regi	4.2
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	4.1
45	400545	NA		Target Exon	4.1
	403051	NA		Target Exon	4.1
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	4.1
	450244	AA007534	Hs.125062	ESTs	4.1
	453261	AA034116	Hs.118494	ESTs	4.1
50	440246	W52010	Hs.191379	ESTs	4.1
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	4.1
	438232	AI150595	Hs.122226	ESTs	4.1
	410233	AA082947		gb:zn10g07.s1 Stratagene hNT neuron (937	4.1
	412179	BE270758	Hs.69428	hypothetical protein MGC3020	4.1
55	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na gluc	4.1
	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	4.1
	453692	AL110416		gb:DKFZp434K0431_r1 434 (synonym: htes3)	4.1
	448640	AW817177	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.1
	417481	AA203281	Hs.21798	ESTs	4.1
60	412912	AW118878	Hs.110835	ESTs	4.1
	454183	AW807116		gb:MR4-ST0062-040100-024-b12 ST0062 Homo	4.1
	426328	AW631296		gb:hh83c09.y1 NCL_CGAP_GU1 Homo sapiens	4.1
	435942	R06285	Hs.191215	ESTs	4.1
	417629	T76945		gb:yc92c07.r1 Soares infant brain 1N1B H	4.1
65	403593	NA		Target Exon	4.0
	402690			Target Exon	4.0
	418190	R49591	Hs.270425	ESTs	4.0

5	408641	AW245207	Hs.5555	hypothetical protein MGC5347	4.0
	427899	AA829286	Hs.332053	serum amyloid A1	4.0
	445975	A1811536	Hs.145734	ESTs	4.0
	438831	BE263273	Hs.6439	synapsin II	4.0
	455578	BE006350	Hs.14355	Homo sapiens cDNA FLJ13207 fls, clone NT	4.0
10	401840	NA		Target Exon	4.0
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	4.0
	445030	AI205925	Hs.147238	ESTs, Highly similar to AAC3_HUMAN ALPHA	4.0
	433873	AW155913	Hs.150478	ESTs, Weakly similar to A Chain A, Cryst	4.0
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	4.0
	450112	BE047734	Hs.5473	ESTs, Moderately similar to ALU5_HUMAN A	4.0
	448906	AI589567	Hs.309719	ESTs	4.0



TABLE 23A

Table 23A shows the accession numbers for those pkeys lacking unigeneID's for Table 23. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey CAT number Accessions

409853	1156226_1	AW502327 AW502488 AW501829 AW502625 AW502687
410034	1170594_1	BE067414 BE067958 BE067419 BE067963 AW577127 AW601412
410233	118656_1	AA082947 AA083036
410490	1206347_1	H03589 AW750687 AW750688
410882	1225686_1	AW809163 AW809247 AW809177 AW809190 AW809225
411478	1247073_1	BE143068 AW849143 AW848705 AW848569 AW848071 AW848475 AW848092 AW848005
413065	1347960_1	BE063555 BE151321 BE151319 BE151657 BE151655 BE063556 BE151322
413072	1348163_1	BE063965 BE063968 BE064034 BE064028 BE063874 BE063966 BE063869 BE064043 BE064033 BE063884
414593	1464909_1	BE386764 BE387560
414913	1506721_1	R25621 C03959 C04010
415011	151328_1	AW963085 AA159005 AW963073
415986	1564410_1	Z43619 R81274 H12206 R12883
416267	1583547_1	H45384 H49125 H41699
417574	1687770_1	R00348 R09593
417629	1690392_1	T76945 R20210 R05755
418556	1767866_1	T02850
419583	186198_1	F00312 AA247490 F31427 AA383663 F22045
426328	264901_1	AW631296 AA375484
439590	47413_1	AF086410 W94386 W74609
442398	541271_1	AA994520 AW393574
452205	90415_1	C15819 AA024741 AA024742
452654	925931_1	BE004783 BE004947 A1911790
453692	977825_1	AL110416 AW876759
454183	1049636_1	AW807116 AW807569 AW807415 AW807338 AW807288 AW807263 AW807316 AW177402 AW807413 AW807068 BE141561 BE141569 AW807401 AW807310 BE141555 AW807318 AW807119 AW807299 AW807241 AW807225 AW807204 AW807345 AW807103 BE141615 AW807431 AW807393 AW807337 AW807406 AW807259 AW807375 AW845890 AW807220 AW807399 AW807064 AW807376 AW807024 BE141595 AW807236 AW807027 AW807112 AW807378 AW807202 BE141593 AW807216 AW807138 AW807244 AW807221 AW807297 AW807050 AW807248 AW807404 AW807075 AW807237 AW807212 AW807308 AW807110 AW807104 BE140912 AW807301 AW807382 AW807294 AW807026 AW807020 AW807108 AW807025 AW807433 AW807124 AW807419 AW807031 AW807264 AW807032 AW807029 AW807052 AW807391 AW807207 AW807215 AW807019 AW807238 AW807201 BE141590 AW807302 AW807323 AW807380 AW807109 BE141588 AW845877 AW807418 AW807407 AW807309 BE141614 AW845861 AW807396 AW807300 AW807348 AW807311 AW807214 AW807132 AW807402 AW807350 AW807028 AW807298 AW807291 AW807305 AW807217 AW807312 AW807261 AW807268 AW807260 AW807266 AW807198 AW807346 AW807315 BE140940 AW807351 AW807122 AW807235 AW807076 AW807314 AW807213 AW807143 AW807131 AW800079 AW807066 AW807077 AW845923 AW807421 BE141619 BE140943 AW807420 AW807381 BE141621 AW845921 BE141629 BE141625 BE141624 BE141636 BE141630 AW807405 AW807290 AW807353
454404	1170594_1	BE067414 BE067958 BE067419 BE067963 AW577127 AW601412
454775	1234106_1	BE160229 AW819879 AW820179 AW819882 AW819876 AW820169 BE153201 AW993735 BE152911
455282	1273020_1	BE143867 AW935060 AW886684
459159	919998_1	A1904646 BE179494 BE179421

**TABLE 23B**

**Table 23B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 23. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
15				
	Pkey	Ref	Strand	Nt_position
	400545	9800107	Minus	124618-124881
	400870	9838306	Minus	34061-35027
20	400973	7980452	Minus	98119-98253
	401093	8516137	Minus	22335-23166
	401590	9966320	Minus	33547-33649
	401665	7145001	Plus	121591-122537
	401810	7342191	Plus	129063-129476
25	401840	7684597	Plus	56283-56439
	402054	8083691	Minus	8288-8806
	402195	7689778	Minus	147901-148884
	402583	7684486	Plus	94883-95003
	402690	8348058	Plus	13368-13998
30	402698	8570304	Minus	108641-108903
	402779	9588555	Minus	38173-39210
	403017	6693623	Plus	78630-78687
	403051	4827080	Minus	5269-5411
	403283	7770677	Plus	52431-52737
35	403433	9719611	Minus	72225-72437
	403593	6862850	Minus	62554-62712,69449-69602
	403612	8469060	Minus	94723-94859
	403921	7711590	Minus	3297-3536
	404368	7630956	Minus	102053-102199
40	404682	9797231	Minus	40977-41150
	404689	7534100	Plus	119461-119717
	405016	6524300	Plus	51997-53308
	405062	7657730	Plus	101283-101432
	406118	9143818	Plus	53997-54629
45	406344	9255974	Plus	20254-20374,20526-20659,20835-21097
	408563	7711604	Plus	34401-34538

TABLE 24:

Table 24 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, Pred.Cell.Loc., and ExAccn for all of the sequences in Table 25. The information in Table 24 is linked by Seq ID No. to Table 25.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 Pred.Cell.Loc.: Predicted Cellular Localization  
 Seq.ID.No.: Sequence Identification Number found in Table 25

	Pkey	ExAccn	UnigeneID	Unigene Title	Pred.Cell.Loc.	Seq. ID. No.
	449746	AI668594	Hs.176586	ESTs, Weakly similar to CP4Y_HUMAN CYTOC		Seq ID 1 & 2
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR		Seq ID 3 & 4
20	415539	AI733881	Hs.72472	BMP-R1B		Seq ID 5 & 6
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278		Seq ID 7 & 8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma		Seq ID 9 & 10
	102457	NM_001394Hs.2359		dual specificity phosphatase 4	nuclear	Seq ID 11 & 12
	429170	NM_001394Hs.2359		dual specificity phosphatase 4	nuclear	Seq ID 11 & 12
25	424399	AI905687	Hs.2533	aldehyde dehydrogenase 9 family, member	cytoplasm	Seq ID 13 & 14
	422505	AL120862	Hs.124165	ESTs		Seq ID 15 & 16
	449765	N92293	Hs.205832	ESTs, Moderately similar to ALU8_HUMAN A		Seq ID 17 & 18
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety		Seq ID 19 & 20
	426215	AW963419	Hs.155223	stanniocalcin 2		Seq ID 21 & 22
30	439840	AW449211	Hs.105445	GDNF family receptor alpha 1		Seq ID 23 & 24
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE		Seq ID 25 & 26
	429220	AW207206	Hs.136319	ESTs		Seq ID 27 & 28
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated		Seq ID 29 & 30
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,		Seq ID 31 & 32
35	442818	AK001741	Hs.8739	hypothetical protein FLJ10879		Seq ID 33 & 34
	442082	R41823	Hs.7413	ESTs		Seq ID 35 & 36
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti		Seq ID 37 & 38
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL		Seq ID 39 & 40
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic		Seq ID 41 & 42
40	442117	AW664964	Hs.128899	ESTs		Seq ID 43 & 44
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA		Seq ID 45 & 46
	429353	AL117406	Hs.200102	ATP-binding cassette transporter MRP8		Seq ID 47 & 48
	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA		Seq ID 49 & 50
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega		Seq ID 51 & 52
45	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR		Seq ID 53 & 54
	423242	AL039402	Hs.125783	DEME-6 protein		Seq ID 55 & 56
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein		Seq ID 57 & 58
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3		Seq ID 59 & 60
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin		Seq ID 61 & 62
50	439569	AW602166	Hs.222399	CEGP1 protein		Seq ID 63 & 64
	114480	BE086778	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polyp		Seq ID 65 & 66
	404561			NM_014112*:Homo sapiens trichostatinophala	mitochondria	Seq ID 67 & 68
	325372	NA		Phase 2 & 3 Exons	nuclear	Seq ID 69 & 70
	112287	AB033064	Hs.334806	KIAA1238 protein		Seq ID 71 & 72
55	335824	NA		ENSP00000249072*:DJ222E13.1 (N-TERMINAL		Seq ID 73 & 74
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family		Seq ID 75 & 76
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin		Seq ID 77 & 78
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph		Seq ID 79 & 80
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	ER	Seq ID 81 & 82
60	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)		Seq ID 83 & 84
	421155	H87879	Hs.102267	lysyl oxidase	extracellular	Seq ID 85 & 86
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy		Seq ID 87 & 88
	420813	X51501	Hs.99949	prolactin-induced protein	nuclear	Seq ID 89 & 90
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr		Seq ID 91 & 92

5	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	cytoplasm	Seq ID 93 & 94
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	nuclear	Seq ID 95 & 96
	429858	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t		Seq ID 97 & 98
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	extracellular	Seq ID 99 & 100
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6		Seq ID 101 & 102
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	extracellular	Seq ID 103 & 104
	424001	W67883	Hs.137476	paternally expressed 10		Seq ID 105 & 106
	421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3		Seq ID 107 & 108
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	nuclear	Seq ID 109 & 110
	419667	AJ077005	Hs.92208	a disintegrin and metalloproteinase doma		Seq ID 111 & 112
15	414812	X72755	Hs.77367	monokine induced by gamma Interferon	extracellular	Seq ID 113 & 114
	426320	W47595	Hs.169300	transforming growth factor, beta 2	extracellular	Seq ID 115 & 116
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	extracellular	Seq ID 117 & 118
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recept		Seq ID 119 & 120
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1		Seq ID 121 & 122
20	428398	AI249368	Hs.98558	ESTs		Seq ID 123 & 124
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane	Seq ID 125 & 126
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4		Seq ID 127 & 128
	412970	AB026436	Hs.177534	dual specificity phosphatase 10		Seq ID 129 & 130
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	extracellular	Seq ID 131 & 132
	415752	BE314524	Hs.78776	putative transmembrane protein		Seq ID 133 & 134
	444051	M48373	Hs.10247	activated leucocyte cell adhesion molecu		Seq ID 135 & 136
	451110	AI955040	Hs.285398	ESTs, Weakly similar to transformation-r		Seq ID 137 & 138

**TABLE 24A**

**Table 24A** shows the accession numbers for those pkeys lacking unigeneID's for Table 24. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10 Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

15 Pkey CAT number Accession  
 335824 CH22\_3197FG\_619\_11\_LINK\_E  
 325372 c12\_hs

TABLE 24B

Table 24B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 24. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NT\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
404561	9795980	Minus	69039-70100

Table 25

The 69 gene sequences identified to be overexpressed in breast cancer may be used to identify coding regions from the public DNA databases (nr and htgs in Genbank). The sequences may be used to either identify genes that encode known proteins, or they may be used to predict the coding regions from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solov'yev, 2000, Genome Res. 10:516-522)

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #:

FGENESH predicted ORF

Coding sequence:

1-1518 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCCT CCTGGCTTCA GGAACATG GCTCACCCCT TCTTGCTGCT GATCCTCCTC 60
TGCATGCTCT TGCTGCTGTT TCAGGTAATC AGGTTGTACC AGAGGAGGAG ATGGATGATC 120
AGAGCCCTGC ACCTGTTTCC TGCACCCCTT GCCCACTGGT TCTATGGCCA CAAGGAGTTT 180
TACCCAGTAA AGGAGTTTGA GGTGTATCAT AAGCTGATGG AAAAAATCCC ATGTGCTGTT 240
CCCTTGTTGGG TTGGACCCCT TACGATGTTT TACGATGTTT ATGACCCAGA CTATGCCAAG 300
ATTCTCCTGA AAAGACAAGA TCCCAAAAGT GCTGTAGGCC AAAAAATCCT TGAATCCTGG 360
GTTGGTGGAG GACTTGTGAC CCTGGATGGT TCTAAATGGA AAAAGCACCG CCAGATTGTG 420
AAACCTGGCT TCAACATCAG CATTCTGAAA ATATTTCATCA CCATGATGTC TGAGAGTGTT 480
CGGATGATGC TGAACAAATG GGAGGAACGC ATTGCCCAAA ACTCACGCTT GGAGCTCTTT 540
CAACATGTCT CCCTGATGAC CCTGGACAGC ATCATGAAAT GTGCCITCAG CCACCAAGGC 600
AGCATCCAGT TGGACAGTAC CCTGGACTCA TACCTGAAAG CAGTGTTCAA CCTTAGCAAA 660
ATCTCCAACC AGCGCATGAA CAATTTTCTA CATCACAACG ACCTGGTTTT CAAATTCAGC 720
TCTCAAGGCC AAATCTTTT TAAATTTAAC CAAGAACITC ATCAGTTTAC AGAGAAAAGTA 780
ATCCAGGACC GGAAGGAGTC TCTTAAGGAT AAGCTAAAAC AAGATACTAC TCAGAAAAGG 840
CGCTGGGATT TTCTGGACAT ACTTTTGAGT GCCAAAAGCG AAAACACCAA AGATTCTCT 900
GAAGCAGATC TCCAGGCTGA AGTGAAAACG TTCATGTTTG CAGGACATGA CACCACATCC 960
AGTGCTATCT CCTGGATCCT TACTGCTTG GCAAAGTACC CTGAGCATCA GCAGAGATGC 1020
CGAGATGAAA TCAGGGAACCT CTAGGGGATG GGGTCTTCTA TTACCTGGGA ACACCTGAGC 1080
CAGATGCCCT ACACCAAGAT GTGCATCAAG GAATGCCCTC GCCTCTACGC ACCGGTAGTA 1140
AACATATCCC GGTACTCTGA CAAACCCATC ACCTTTCCAG ATGGACGCTC CTTACCTGCA 1200
GGAATAACTG TGTATTATCA TATTGGGCTT CTTACCACCA ACCCTATTTT CTGGGAAAGC 1260
CCTCAGGTCT TTAACCCCTT GAGATTCTCC AGGGAAAAAT CTGAAAAAAT ACATCCCTAT 1320
GCCTTCATAC CATTCTCAGC TGGATTAAGG AACTGCATTG GGCAGCAATT TGCCATAATT 1380
GAGTGTAAGG TGGCAGTGGC ATTAACCTCT CTCCGCTTCA AGCTGGCTCC AGACCACTCA 1440
AGGCCTCCCC AGCCTGTTCG TCAAGTTGTC CTCAGTCCA AGAATGGAAT CCATGTGTTT 1500
GCAAAAAAAG TTGCTAATT TTAAGTCCCT TCGTATAAGA ATTAATGAGA CAATTTCTCT 1560
ACCAAAGGAA GAACAAAAGG ATAAATATAA TACAAAATAT ATGTATATGG TTGTTTGACA 1620
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TGCGAAGGGA AATTATGGT TGTGTAACT AGTGGTAGAG TGGCTTTCAA GCATAGTTTG 1800
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Seq ID NO: 2 Protein sequence

Protein Accession #:

FGENESH predicted

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VGRGLVTLDG SKWKHRQIV KPGFNISLK IFITMSESV RMMLNKWEER IAQNSRIELF 180
QHVSLMTLDS IMKCAFSHQG SIQLDSTLDS YLKA VFNLSK ISNQRMNFL HHNDLVFKFS 240
SQGQIFSKFN QELHQFTEKV IQDRKESLKD KKKQDITQKR RWDPLDILLS AKSENTKDFS 300
EADLQAEVKT FMFAGHDTTS SAISWLYCL AKYPEHQORC RDEIRELLGD GSSITWHLS 360
QMPYTIMCIK ECLRLYAPVV NISRLDKPI TFPDGRSLPA GITVFINWA LHHNPYFWED 420
PQVFNPLRFS RENSEKIHPY AFIPFSAGLR NCIGQHFAII ECKVAVALTL LRFKLAPDHS 480
RPPQVVRQVV LKSKNGIHFV AKKVC

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Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #:

NM\_052997

Coding sequence:

100-4125 (underlined sequences correspond to start and stop codons)

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ATTCTGATAG ATTCTGGTGC CGATATAAAT CTCGTAGATG TGTATGGCAA CATGGCTCTC 360
CATTATGCTG TTTATGTGCA GATTGTGCA GTGGTGGCAA AACTGCTGTC CCATGGTGCA 420
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 Protein Accession #: NP\_443723.1

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CGVTAEHYAV TCGFHHIHEQ IMEYIRKLSK NHQNTNPEGT SAGTPDEAAP LAERTPDAT 240  
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 IAWKKETPV KTGCVARVTS NKTKVLEKGR SKMIACPTKE SSTKASANDQ RFPSESKQEE 420  
 DEEYSCDSRS LFESSAKIQV CIPESIQKV MEINREVEEP PKKPSAFKPA IEMQNSVPNK 480  
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 KLEESPNKDG LLKATCGMKV SIPTKALELK DMQTFKAEP GKPSAFEPAT EMQKSVNKA 600  
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 DIELKSVEEN LNQVSHHEN ENYLLHNCM LKKEIAMLKL EIATLKHQYQ EKENKYFEDI 1080  
 KILKEKNAEL QMTLKLKES LTKRASQYSG QLKVLIAENT MLTSKLEBKQ DKEILEABIE 1140  
 SHHPRLASAV QDHDQVTSR KQEPAFHIA GDAQLQRKMN VDVSTIYNN EVLHQLPSEA 1200  
 QRKSKSLKIN LNYAGDALRE NTLVSEHAQR DQRETQCMK BAEHMYQNEQ DNVNKHTEBQ 1260  
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Seq ID NO: 5 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 273-1785 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 6 Protein sequence:

Protein Accession #: none found

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 EQSQSSSGS GLPLLVRTI AKQIQMVQI GKGRYGEVVM GKWRGEKVA VVFFTTBEAS 240  
 WPRETIVQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNLV KNGTCCAD LGLAVKFSID 360  
 TNEVDIPNT RVGTKRYMPP EVLDESNNRN HFQSYIMADM YSFGLLWEV ARRCVSGGIV 420

EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480  
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Seq ID NO: 7 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 482-3007 (underlined sequences correspond to start and stop codons)

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60 TTTTGAACCT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAAGTCC TGGAGCAGCA 3000  
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65 GCATTATCTT CAGGCAATTT AGTCTGTCCC AAATAAAATC AATCTTGCA TGTAATC

Seq ID NO: 8 Protein sequence:

Protein Accession #: none found

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75 IFVPLTHLDL RGNQLQTLFY VGFLBHGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS 240  
RIGDVVCNSP PFFKGSILSR LKESICPTP PVYBEHEDPS GSLHLAATSS INDSRMSTKT 300  
TSILKLPTKA PGLPIYITPK STQLPGPYCP IPCNCKVLSP SGLLIHQER NIESLSDLRP 360

PFQNPRLKIL AGNIHSLMK SDLVEYFTLE MLHLGNRRJE VLEEGSFMNL TRLOKLYLNG 420  
 NHLTKLSKGM FLGLHNLLEYL YLEYNAIKEI LPTGFNPMK LKVLVYLNLL LQVLPPIHS 480  
 GVPLTKVNLK INQFTHLPVS NILDDLDDLT QIDLEDNPWD CSCDLVLQOQ WIKLSKNTV 540  
 TDDILCTSPG HLDKKEKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNTADTILRS 600  
 1 LTAIVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KQVDEQMRD NSPVHLQYSM 660  
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 10 LLEQENHSPL TGSNMKYKIT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA 780  
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Seq ID NO: 9 DNA sequence

Nucleic Acid Accession #: NM\_003474

Coding sequence: 307-3036 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CACTAACGCT CTTCCTAGTC CCCGGGCCAA CTCGGACAGT TTGCTCATT ATTGCAACGG 60  
 TCAAGGCTGG CTGTGCCAG AACGGCGCGC GCGCGACGCA CGCACACACA CGGGGGGAAA 120  
 20 CTTTTTTAAA AATGAAAGGC TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCGAGGGCT 180  
 CCGGAGCTGA CTCGCCGAGG CAGGAAATCC CTCGGTCTGC GACGCCCGGC CCGCTCGGC 240  
 GCGCGGTGG GATGGTGCAG CGCTGCGCGC CGGGCCCGAG AGCTGCTGCA CTGAAGGCCG 300  
 GCGACGATGG CAGCGCGCCC GCTGCGCGTG TCCCCCGCCC GCGCCCTCCT GCTGCGCCCTG 360  
 GCGGTGCTG TGCTGCGGCC CTGCGAGGCC CGAGGGGTGA GCTTATGGAA CGAAGGAAGA 420  
 25 GCTGATGAAG TTGTCAGTGC CTCTGTTCCG AGTGGGGACC TCTGGATCCC AGTGAAGAGC 480  
 TTCGACTCCA AGAATCATCC AGAAGTGTG AATATTGAC TACAACGGGA AAGCAAAGAA 540  
 CTGATCATAA ATCTGGAAAG AAATGAAGGT CTCATTGCCA GCAGTTTCAC GGAAACCCAC 600  
 TATCTGCAAG ACGGTACTGA TGTCTCCCTC GCTCGAAAT ACACGGTAAT TCTGGGTAC 660  
 TGTTACTACC ATGGACATGT ACGGGGATAT TCTGATTCAG CAGTCAGTCT CAGCACGTGT 720  
 30 TCTGGTCTCA GGGGACTTAT TGTGTTTGA AATGAAAGCT ATGTCTTAGA ACCAATGAAA 780  
 AGTGAACCA ACAGATACAA ACTCTTCCA CGAAGAAGC TGAAGCGT CCGGGGATCA 840  
 TGTGGATCAC ATCACAACAC ACCAAACCTC GCTGCAAGA ATGTGTTCC ACCACCTCT 900  
 CAGACATGGG CAAGAAGGCA TAAAGAGAG ACCCTCAAGG CAACTAAGTA TGTGGAGCTG 960  
 GTGATCGTGG CAGACAACCG AGAGTTTCAG AGGCAAGGAA AAGATCTGGA AAAAGTTAAG 1020  
 35 CAGCGATTAA TAGAGATTGC TAATCAGTT GACAAGTTT ACAGACCACT GAACATTCGG 1080  
 ATCGTGTGG TAGGCGTGA AGTGTGGAAT GACATGGACA AATGCTCTGT AAGTCAGGAC 1140  
 CCATTCACCA GCCTCCATGA ATTCTGAC TGGAGGAAGA TGAAGCTCT ACCTCGCAAA 1200  
 TCCCATGACA ATGCGCAGCT TGTGAGTGG GTTATTTC AAGGGACCAC CATCGGCATG 1260  
 GCGCCCAATG TAGACATGT CAGGCGAGAC CAGTCTGGGG GAATTGTCAT GGACCATTC 1320  
 40 GACAAATCCC TTGTGTCAGC CGTGACCCTG GCACATGAGC TGGGCCACAA TTTCGGGATG 1380  
 AATCATGACA CACTGGACAG GGGCTGTAGC TGTCAATGG CGTTGAGAA AGGAGGCTGC 1440  
 ATCATGAACG GTCCACCGG GTACCCATT CCCATGGTGT TCAGCAGTTG CAGCAGGAAG 1500  
 GACTTGGAGA CCAGCTTGA GAAAGGAATG GGGGTGTGCC TGTTTAACCT GCCGGAAGTC 1560  
 AGGGAGTCTT TCGGGGGCCA GAAGTGTGG AACAGATTG TGAAGAAGG AGAGGAGTGT 1620  
 45 GACTGTGGGG AGCCAGAGGA ATGTATGAAT CGCTGTGCA ATGCCACCAC CTGTACCCTG 1680  
 AAGCCGACG CTGTGTGCGC ACATGGGCTG TGCTGTGAAG ACTGCCAGCT GAAGCCTGCA 1740  
 GGAACAGCGT GCAGGACTC CAGCAACTCC TGTGACCTCC CAGAGTCTG CACAGGGGCC 1800  
 AGCCCTCACT GCCCAGCCA CGTGTACCTG CACGATGGGC ACTCATGTCA GGATGTGGAC 1860  
 GGCTACTGCT ACAATGGCAT CTGCCAGACT CACGAGCAGC AGTGTGTAC ACTCTGGGGA 1920  
 50 CCAGGTGCTA AACCTGCCCT TGGGATCTGC TTTGAGAGAG TCAATTCTGC AGGTGATCCT 1980  
 TATGGCAACT GTGGCAAGT CTCGAAGAGT TCCTTTGCCA AATGCGAGAT GAGAGATGCT 2040  
 AAATGTGGA AAATCCAGTG TCAAGGAGGT GCCAGCGGC CAGTCATTGG TACCAATGCC 2100  
 GTTTCCATG AAACAACAT CCCCTGCA GCAAGGAGGC GGATTCTGT CCGGGGGACC 2160  
 CACGTGTACT TGGGCGATGA CATGCCGGAC CCAGGGCTTG TGCTTGCAG CACAAAGTGT 2220  
 55 GCAGATGGA AAATCTGCCT GAATCGTCAA TGTCAAAATA TTAGTGTCT TGGGGTTTAC 2280  
 GAGTGTGCAA TGCAGTGCCA CGGCAGAGGG GTGTGCAACA ACAGGAAGAA CTGCCACTGC 2340  
 GAGGCCCACT GGGCACCTCC CTTCGTGAC AAGTTTGCT TGGAGGAAG CACAGACAGC 2400  
 GGCCCATCC GGCAAGCAGA TAACCAAGGT TTAACCATAG GAAITCTGT GACCATCCTG 2460  
 TGTCTTCTG CTGCCGATT TGTGTTTAT CTCAAAAGGA AGACCTTGAT ACGACTGCTG 2520  
 60 TTTACAAATA AGAAGACCAC CATTGAAAAA CTAAGGTGTG TGGCCCTTC CCGGCCACCC 2580  
 CGTGGCTTCC AACCTGTCA GGCTCACCTC GGCCACCTTG GAAAAGGCCT GATGAGGAAG 2640  
 CCGCCAGATT CCTACCCACC GAAGGACAA CCCAGGAGAT TGCTGCAGTG TCAGAAATGT 2700  
 GACATCAGCA GACCCCTCAA CGGCTGAAT GTCCCTCAGC CCCAGTCAAC TCAGCGAGTG 2760  
 CTCTCTCCCC TCCACCGGGC CCCACGTGCA CTTAGCGTCC CTGCCAGACC CCGCCAGCC 2820  
 65 AAGCCTGCA TTAGCGAGG CCAGGGGACC TGTAAAGCAA ACCCCCTCA GAAGCCTCTG 2880  
 CCTGCAGATC CTCGTGCCAG ACAAACCTCG CTCACTCATG CCTTGGCCAG GACCCAGGA 2940  
 CAATGGGAGA CTGGGCTCCG CCGGCCACC CTCAGACCTG CTCACAAATA TCCACACCAA 3000  
 GTGCCAGAT CCACCCACAC CGCCTATATT AAGTGAAGA CCGACACCT TTTTCAACAG 3060  
 TGAAGACAGA AGTTTGCAT ATCTTCAGC TCCAGTTGGA GTTTTTTGA CCAACTTTTA 3120  
 70 GGATTTTTT TAATGTTAA AACATCATT CTATAAGAAC TTGAGCTAC TGCCGTCAGT 3180  
 GCTGTGCTGT GCTATGGTG TCTGTCTACT TGCACAGGTA CTGTAAAT ATTAAATTTAT 3240  
 GCAGAAATGT GATTACAGTG CAGTGCCTG TAGTAGGCAT TTTTACCATC ACTGAGTTT 3300  
 CCATGGCAGG AAGGCTTGT GTGCTTTTAG TATTTAGTG AACTTGAAT ATCCTGCTTG 3360  
 ATGGGATTCT GAGCAGGATG TGTGTGCTT CTGATCAAGG CCTTATTGGA AAGCAGTCCC 3420  
 75 CCAACTACCC CCAGCTGTGC TTATGGTACC AGATGCAGCT CAAGAGATCC CAAGTAGAAT 3480  
 CTCAGTTGAT TTCTGTGATT CCCCATCTCA GGCCAGAGCC AAGGGGCTTC AGGTCCAGGC 3540  
 TGTGTTTGGC TTTACGGAG CCCTGTGTC CCTTGACAAC TGGCAGGCAG GCTCCAGGG 3600

ACACCTGGGA GAAATCTGGC TTCTGGCCAG GAACTTTGG TGAGAACCTG GGTTCAGAC 3660  
 AGGAATCTTA AGGTGTAGCC ACACCAGGAT AGAGACTGGA AACTAGACA AGCCAGAAT 3720  
 TGACCTGTAG CTGACCAGCC GTGAGCATGT TTGGAAGGGG TCTGTAGTGT CACTCAAGGC 3780  
 GGTGCTTGAT AGAAATGCCA AGCACTTCTT TTTCTCGCTG TCCTTTCTAG AGCACTGCCA 3840  
 5 CCACTAGGTT ATTTAGCTTG GGAAAGGTGG TGTTCCTGTA AGAAACCTAC TGCCAGGCA 3900  
 CTGCAAAACCG CCACCTCCCT ATACTGCTTG GAGCTGAGCA AATCACCACA AACTGTAATA 3960  
 CAATGATCCT GTATTACAGC AGATGAGGAC TTCCATGGG ACCACAATA TTTTCAGATG 4020  
 10 TGAACCATTA ACCAGATCTA GTCAATCAAG TCTGTTACT GCAAGGTTCA ACTTATTAAC 4080  
 AATTAGGCAG ACTCTTATG CTGCAAAAA CTACAACCA TGGAAATGTA TGTTCATGGG 4140  
 TATAGTTCAT GTCTGCTATC ATTATCTGTA GATATTGGAC AAAGAACCCT CTCTATGGGG 4200  
 CATCCTCTTT TTCCAACITG GCTGCAGGAA TCTTTAAAG ATGCTTTTAA CAGAGTCTGA 4260  
 ACCTATTCTT TAAACACTTG CAACCTACCT GTTGAGCATC ACAGAATGTG ATAAGGAAAT 4320  
 CAACITGCTT ATCAACTGCC TAAATATTAT GAGATGTGGC TTGGGCAGCA TCCCTTGAA 4380  
 15 CTCTTCACCT TCAAAATGCC TGACTAGGGA GCCATGTTT ACAAGGTCCT TAAAGTGACT 4440  
 AATGGCATGA GAAATACAAA AATACTCAGA TAAGGTAAAA TGCCATGATG CCTCTGCTT 4500  
 CTGGACTGGT TTTCACATTA GAAGACAAT GACAACAGT ACATAATTCA CTCTGAGTGT 4560  
 TTTATGAGAA AGCCTCTCTT TGGGGTCAAC AGTTTTCCTA TGCTTTGAAA CAGAAAAATA 4620  
 TGTACCAAGA ATCTTGCTT GCCTTCCAGA AAACAAAACT GCATTTTACT TTCCCGGTGT 4680  
 TCCCACTGT ATCTAGGCAA CATAGTATTC ATGACTATGG ATAACTAAA CACGTGACAC 4740  
 20 AAACACACAC AAAAGGGAAC CCAGCTCTAA TACATTCCTA CTCTATAGC ATGCATCTGT 4800  
 TTATCTATA GTTATTAAGT TCTTTAAAT GTAAAGCCAT GCTGGAAAAT AATACTGCTG 4860  
 AGATACATAC AGAATTACTG TAACTGATTA CACTTGGTAA TTGTACTAAA GCCAACATA 4920  
 TATATACTAT TAAAAAGGTT TACAGAATTT TATGTTGAT TACGTGGGCA TTGCTTTTT 4980  
 25 AGATGCCCAA ATCCTTAGAT CTGGCATGTT AGCCTTCCT CCAATTATA GAGGATATGA 5040  
 ACCAAAAAAA AAAAAAAAAA AA

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP\_003465.2

1 11 21 31 41 51  
 MAARPLPVP ARALLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSG DLWIPVKSFD 60  
 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDSLAR NYTVILGHYC 120  
 35 YHGHVRGYS DSAVSLSTCSG LRGLVFEFE SYVLEPMKSA TNRYKLPAP KLKSVRGSCG 180  
 SHHINTPLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240  
 LIEIANHVDK FVRPLNRIV LVGVEVWDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300  
 DNAQLVSGVY FQGTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360  
 40 DTLDRGCSQ MAYEKGGCDM NASTGYFFPM VFSSCSRKDL BTSLEKGMGV CLFNLPEVRE 420  
 SFGGQKQGNR FVEEGEECDG GEPEECMNRC CNATTCITLP DAVCAHGLCC EDCQLKPAQT 480  
 ACRDSSNSCD LPEFTGASP HCPANVYLHD GHSCQDVG DY CYNGICQTHE QQCVTWLPFG 540  
 AKPAPGICFE RVNSAGDPYG NGKGVSKSSF AKCEMRDAKC GKIQCCGGAS RPIVIGNAVS 600  
 IETNPLQQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQ NISVFGVHEC 660  
 45 AMQCHGRGVC NNRKNCHEBA HWAPPFCDKF GFGGSTDSGP IRQADNQLT IGLVITLCL 720  
 LAAGFVVYLK RKTILRLFT NKKTTIEKLR CVRPSRPPRG FQPCQAHLG LGKGLMRKPP 780  
 DSYPPKDNPR RLLQCNQVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAP VPARPLPAK 840  
 ALRQAQGTCK PNPPQKPLPA DPLARTIRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900  
 RSTHTAYIK

Seq ID NO: 11 DNA sequence

Nucleic Acid Accession #: NM\_001394

Coding sequence: 400-1584 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGCACGAGGG CTGAGCGCGG GAGGAGCGTA GGCAGGGCAG CGCTGGCGCC AGCGGCGACA 60  
 GGAGCCGCGC GACCGGCAAA AATACACGGG AGGCCGTCGC CGAAAAGAGT CCGCGGTCCT 120  
 CTCTCGTAAA CACACTCTCC TCCACCGGCG CTTCCCTCTC CGCTCTGCGC GCGCGCCGCG 180  
 60 TGGGCGCGCG AGGCCGCTCC GACTGCTATG TGACCGCGAG GCTGCGGGAG GAAGGGGACA 240  
 GGAAGAAGA GGCTCTCCCG CGGGAGCCCT TGAGGACCAA GTTTGCGGCC ACTTCTGCAG 300  
 GCGTCCCTTC TTAGCTCTCG CTTGCCCTTT TCTGCAGCCT AGCGCGCCCA GGTTCCTTC 360  
 TCTTCTCTCG GCGCCAGCGC GCCTCGGTTT CCGGCGACCA TGGTGACGAT GGAGGAGCTG 420  
 CGGGAGATGG ACTGCAGTGT GCTCAAAAGG CTGATGAACC GGGACGAGAA TGGCGCGCGC 480  
 65 GCGGGCGGCA GCGGCGAGCA CGGCACCTG GGGCTGCCGA GCGGCGGCAA GTGCTGCTG 540  
 CTGGACTGCA GACCGTTCTT GCGGCACAGC GCGGGCTACA TCTAGGTTT GGTCAACGTG 600  
 CGCTGTAAAC CATCTGTGCG GCGGCGGGCT AAGGGCTCCG TGAGCCTGGA GCAGATCCTG 660  
 CCGGCGGAGG AGGAGGTACG CGCCCGCTTG CGCTCCGCGC TCTACTCGGC GGTCTGCTC 720  
 TACGACGAGC GCAGCCGCGC GCGCGAGAGC CTCGCGGAGG ACAGACCGT GTGCTGCTG 780  
 GTGCAGGCGC TGCGCCGCAA CGCGGAGCGC ACCGACATCT GCCTGTCTAA AGCGGGCTAT 840  
 70 GAGAGGTTTT CCTCCAGTA CCCAGAATTC TGTCTAAAA CCAAGGCCCT GGCAGCCATC 900  
 CCACCCCGCG TTCCCGGAG CGCCACAGAG CCCTTGAGCC TGGGCTGCAG CTCTCTGCG 960  
 ACCCCACTAC ACCACCGAGG GGGTCTCTGT GAGATCTTCT CTTCTCTCTA CTTCCGCGAGT 1020  
 GCCTACCATG CTGCGCGGAG AGACATGCTG GACGCGCTTG GCATCACGGC TCTGTTGAAT 1080  
 GTCTCTCTCG ACTGCCCAAA CCACCTTGAA GGACACTATC AGTACAAGT CATCCAGTG 1140  
 75 GAAGATAACC ACAAGGCCGA CATCAGCTCC TGGTTCTATG AAGCCATAGA GTACATCGAT 1200  
 GCGGTGAAGC ACTGCGGTGG GCGCGTCTG GTGCACTGCC AGGCGGGCAT CTCGCGGTCTG 1260  
 GCCACCATCT GCCTGGCCTA CTTGATGATG AAGAAACGGG TGAGGCTGGA GGAGGCTTC 1320

GAGTTCGTGA AGCAGCGCCG CAGCATCATC TCGCCCAACT TCAGCTTCAT GGGGCAGCTG 1380  
 CTGCACTTCG AGTCCCAGGT GCTGGCCACG TCCTGTGCTG CGGAGGCTGC TAGCCCTCG 1440  
 GGACCCCTGC GGGAGCGGGG CAAGACCCCC GCCACCCCA CCTCGCAGTT CGTCTTCAGC 1500  
 TTTCCGGTCT CCGTGGGCGT GCACTCGGCC CCCAGCAGCC TGCCCTACCT GCACAGCCCC 1560  
 ATCACCACCT CTCCCAGCTG TTAGAGCCGC CCTGGGGGCC CCAGAACCAG AGCTGGCTCC 1620  
 CAGCAAGGGT AGGACGGGCC GCATGCGGCA GAAAGTTGGG ACTGAGCAGC TGGGAGCAGG 1680  
 CGACCGAGCT CCTTCCCAT CATTCTCCT TGGCCAACGA CGAGGCCAGC CAGAATGGCA 1740  
 ATAAGGACTC CGAATACATA ATAAAGCAA ACAGAACACT CCAACTAGA GCAATAACCG 1800  
 GTGCGGCAGC AGCCAGGAA GACCTTGGTT TGGTTTATGT GTCAGTTTCA CTTTCCGAT 1860  
 AGAAATTTCT TACCTCATTT TTTAAGCAG TAAGGCTTGA AGTGATGAAA CCCACAGATC 1920  
 CTAGCAAATG TGCCCAACCA GCTTACTAA AGGGGGAGGA AGGGAGGGCA AAGGGATGAG 1980  
 AAGACAAGTT TCCAGAAGT GCCTGGTCT GGGTACTTGT CCTTTTGTG TCGTTGTGT 2040  
 AGTTAAAGGA ATTTCAATTT TAAAGAAAT CTTCGAAGGT GTGGTTTCA TTTCTCAGTC 2100  
 ACCAACAGAT GAATAATTAT GCTTAATAAT AAAGTATTTA TTAAGACTTT CTTCAGAGTA 2160  
 TGAAAGTACA AAAAGTCTAG TTACAGTGA TTAGAATAT ATTTATGTTG ATGTCAAACA 2220  
 GCTGAGCACC GTAGCATGCA GATGTCAAGG CAGTTAGGAA GTAAATGGTG TCTGTAGAT 2280  
 ATGTGCAAGG TAGCATGATG AGCAACTTGA GTTTGTTGCC ACTGAGAAGC AGGCGGGTTG 2340  
 GGTGGGAGGA GGAAGAAAGG GAAGAATTAG GTTTGAATTG CTTTAAAAA AAAAAAGAAA 2400  
 AGAAAAAGAC AGCATCTCAC TATGTGCCA AGGCTCATCT TGAGAAGCAG GCGGGTTGGG 2460  
 TGGGAGGAGG AAGAAAGGA AGAATTAGGT TTGAATTGCT TTTTAAAAA AAAA

Seq ID NO: 12 Protein sequence:

Protein Accession #: NP\_001385

1 11 21 31 41 51  
 | | | | |  
 MVTMEELREM DCSVLKRLMN RDENGGGAGG SGSHGTLGLP SGGKCLLLDC RPFLAHSAGY 60  
 ILGSVNVRCN TIVRRRAKGS VSLEQLPAE BEVRARLRSG LYSVIVYDE RSPRAESLRE 120  
 DSTVSLVQQA LRRNAERTDI CLLKGGYERF SSEYPEFCSE TKALAAAPP VPSPATEPLD 180  
 LGSSCGTPL HDQGGPVIEL PFLYLGSAHY AARRDMLDAL GITALLNVSS DCPNHFEGHY 240  
 QYKCPVEDN HKADISSWFM EAIYIDAVK DCRGRVLVHC QAGISRSATI CLAYLMMKKR 300  
 VRLEAEFEFV KQRSIIIPN PSFMGQLQF ESQVLATSCA AEAASPSGPL RERKTPATP 360  
 TSQVFVSPVP SVGVHSAPSS LPYLHSPITT SPSC

Seq ID NO: 13 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 68-340 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 AGCGCCTTGC CTCTCTTAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60  
 CACCACCATG AAGTCTTAG CAGTCCTGGT ACTCTTGGGA GTTCCATCT TCTTGGTCTC 120  
 TGCCAGAAAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCCTGCTGA 180  
 TGATGAAGCC CCGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240  
 TACCACTGCA ACCACCGCTG CTCTACCACT TGCTCGTAAA GACATTCCAG TTTTACCCAA 300  
 ATGGGTTGGG GATCTCCGGA ATGGTAGAGT GTGTCCTGA GATGGAATCA GCTTGAAGTCT 360  
 TCTGCAATTG GGTCACAACT ATTCATGCTT CCGTGATTT CATCCAACTA CTTACCTTGC 420  
 CTACGATATC CCCTTTATCT CTAATCAGTT TATTTCTTT CAAATAAAAA ATAACATGA 480  
 GCGAGCTAAC AT

Seq ID NO: 14 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51  
 | | | | |  
 MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETTAAA TTATTAAPT 60  
 ATTAASTTAR KDIPVLPKWV GDLPNGRVCP

Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #: NM\_016640.2

Coding sequence: 39-1358 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GCTTAAAGTTG ACCTCTGGGT CCGGAATCGC GGGCAAAGAT GCGGGCGGCC AGGTGTTGGA 60  
 GGCCTTTGCT ACGCGGTCCG AGGCTTTTCA TGCACACCGC GGCTAATGCC GCGGCCACGG 120  
 CTACAGAAAC GACCTCCCAA GACGTGCGCG CGACCCCGT CCGCGGTAC CCGCCGATTG 180  
 TGCCCTCCAT GACAGCCGAC AGCAAAGCTG CACGGCTGCG GCGGATCGAG CGCTGGCAGG 240  
 CGACGGTGCA CGCTGCGGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCACT 300  
 TTATGAAGTA CATGGTTTAC CCGCAGACCT TCGCACTGAA TGCCGACCGC TGGTACCACT 360  
 ACTTCACCAA GACCGTGTTC CTGTGGGTC TGCCGCGGCC CCCAGCGGAG CCGGAGCCCG 420  
 AGCCCCAACC CGAACTGGA CCGCGCTGG ACCTCGCGGC GCTGCGTGCG GTGCGCTGCG 480  
 ACTGCTGCT GCAGGAGCAC TTCTACCTGC GCGCAGGCG GCGCGTGAC CGTTACGAGG 540

5 AGAGCGAGGT CATATCTTTG CCTTCCTGG ATCAGCTGGT GTCAACCTC GTGGGCTCC 600  
 TCAGCCCA CAACCCGCC CTGGCCGCTG CCGCCCTCGA TTATAGATGC CCAGTTCATT 660  
 TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCGTGGTCA TCGAAGAGGT CGAATTGATG 720  
 ACTTGGGATA CCAGATAGAT GATAAACCAA ACAACCAGAT TCGAATATCC AAGCAACTCG 780  
 CAGAGTTTGT GCCATTGGAT TATTCTGTTT CTATAGAAAT CCCCACTATA AAATGTAAAC 840  
 CAGACAAACT TCCATTATTC AAACGGCAGT ATGAAAACCA CATATTTGTT GGCTCAAAAA 900  
 CTGCAGATCC TTGCTGTTAC GGTACACACC AGTTTCATCT GTTACCTGAC AAATTAAGAA 960  
 GGGAAAGGCT TTGAGACAA AACTGTGCTG ATCAGATAGA AGTTGTTTIT AGAGCTAATG 1020  
 CTATTGCAAG CCTTTTGTCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG 1080  
 AAGCAGATGT TACTCGACCT TTTGTCTCCC AGGCTGTGAT CACAGATGGA AAATACTTTT 1140  
 CCTTTTCTG CTACCAGCTA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAAATAACC 1200  
 CTCGTAAAAA TATATGTTGG GTACACAAA GTAAGCCTCT TTATGAAACA ATTGAGGATA 1260  
 ATGATGTGAA AGGTTTAAAT GATGATGTTT TACTTCAGAT AGTTCACTTT CTACTGAATA 1320  
 GACCAAAAGA AGAAAAATCA CAGCTGTGGG AAAACTGAAA AAGCATATTT GATTGAGAAC 1380  
 15 TGTGGGAATA TTAAATTTT ACTGAAGGAA CAATAATGAT GAGATTGTA ACTGTCAACT 1440  
 ATTAATACA TTGATTTTGT AGACAAATAT TTCTTATGTC AACCTGTTAT TAGATCTCTT 1500  
 ACTCTGCTCA AATTCATCAC TGAAGAGATT AATTITAGTT ACCTTTTGTI GATTIAAAAA 1560  
 TAATTGCATT TGTAATTTGC TAACGTATAA GACAAATTGA GTTATTGAGC TATTAATGTC 1620  
 20 ACATTTAAT ATAAATGCAG AAATCCCAAA TAAATGCTA ACATACTGAA TTCAGTAATT 1680  
 AAAAGAACCC ACTGC

Seq ID NO: 16 Protein sequence:

Protein Accession #: NP\_057724.1

25 1 11 21 31 41 51  
 MAAARCWRLP LRGPRLSLHT AANAATATE TTSQDVAATP VARYPPIVAS MTADSKAARL 60  
 RRIRRWQATV HAAESVDEKL RILTKMQFMK YMVVYQTFAL NADRWYQYFT KTVFLSGLPP 120  
 30 PPAEPPEPE PEPEPALDLA ALRAVACDCL LQEHFVLRRL RRVRHYEES VISLPFLDQL 180  
 VSTLVGLLSP HNPALAAAAA DYRCPVHFYW VRGEEHPRG HRRGRIDDLR YQIDDKPNNQ 240  
 IRISKQLAEF VPLDYSVPIE IPTIKCKPDK LPLFKRQYEN HIFVGSKTAD PCCYGHGTQFH 300  
 LLPDKLRRLR LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQGFWEAD VTRPFVSQAV 360  
 35 ITDGKYFSFF CYQLNTLALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDDEVLLQ 420  
 IVHFLNRPK EEKSQLEEN

Seq ID NO: 17 DNA sequence

Nucleic Acid Accession #: NM\_025059.1

Coding sequence: 3-2150 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 GCATGAGCCT GGAAGTGCAC AGCCATATCG CGCTGGGTGC CGCTTCGCCA GCGCCCGAGG 60  
 45 AAACCTACGA TCATCTTTTG GAAGTCCCGG TCACGCGGGA GCAGTTAAAC CACTATCGGA 120  
 ATGTGGCTCA AAATGCTCGA AGTGAACCTT CAGCAACTTT GGTCAAAATT GAATGTGCTC 180  
 AGTCTGAGCT TCAAGACCTC CGATCCAAGA TGCTTTCTAA AGAAGTCTCC TGTCAAGAAC 240  
 TGAAAGCTGA AATGGAGAGC TACAAGGAAA ACAATGCCAG AAAATCATCT CTCCTTACCT 300  
 CTTTGAGAGA CAGAGTTCAG GAACTAGAAAG AAGAATCAGC AGCACTTCC ACTTCTAAAA 360  
 50 TCAGAACAGA AATCACAAGT CACGCTGCAA TCAAGGAGAA CCAGGAATTA AAGAAGAAAG 420  
 TTGTAGAGTT AATGAAAAA TTACAAAAGT GTTCAAAAAGA AAATGAGGAG AATAAGAAAC 480  
 AAGTTTCAAA GAATTGCAGG AAACATGAGG AATTCTGAC TCAACTGCGT GACTGCTTGG 540  
 ATCCAGATGA GAGGAATTAC AAGCATCAG ATGAAGATT AATTTTAAAG CTTAGAGACC 600  
 55 TGCGCAAAGA AAATGAATTC GTGAAAGGAC AAATTGTTAT TCTTGAAGAG ACTATAAATG 660  
 TCCATGAGAT GGAAGCAAAA GCTAGCAGAG AAACGATCAT GAGGCTGGCT TCAGAAAGTCA 720  
 ACAGAGAGCA GAAAAAAGCT GCCTCCTGTA CTGAAGAGAA AGAGAAGCTG AACCAAGGACC 780  
 TGCTCAGTGC TGTAGAAGCA AAAGAAGCTC TTGAAAGGGA AGTTAAGATC TTCCAAGAAA 840  
 GGCTGCTTGC TGGCCAGCAG GTCTGGGATG CCTCAAGCA GGAAGTGAGC CTCTGAAGA 900  
 60 AAAGCTCTTC TGAGTTGGAG AAGAGTTTGA AGGCCAGTCA GGATGCAGTC ACAACCTCAC 960  
 AAAGCCAGTA CTCCTCATT AGGGAGAAAA TCGCAGCCCT CCTTAGGGGC AGATTGAGCA 1020  
 TGACTGGGTC CACTGAGGAC ACCATTTTGG AGAAGATTCT AGAAATGGAC AGCCGGGAAG 1080  
 AAAGCAGGGA CCGGATGGTC TCCAGCTTG AAGCCCAAAT ATCTGAGCTT GTTGAACAGT 1140  
 TGGGAAAGGA GTCTGGGTTT CACCAGAAAG CTCTCCAGAG GGCCAGAAA GCAGAGAATA 1200  
 65 TGTGAGAGAC TCTCAGGGT CAGCTGACAC ACCTGGAGGC AGAGCTGGIT TCTGGAGGTG 1260  
 TTTTGGGAGA CAACTTGAAT TTTGAGAAA AAAAAATATCT TAAATTTCTG GATCAGCTTT 1320  
 CTCAGAAAAT GAAGTTGGAC CAGATGGCTG CCGAACTTGG CTTGACACG CGGCTGGACG 1380  
 TGGTTTTAGC TCGAACAGAG CAGCTGGTTC GTCTTGAGAG CAATGCAGTC ATTGAGAACA 1440  
 AGACCATTTG CCACAATTTC CAGAGAAAGC TAAAGACACA GAAAGAGAGA CTGGAGAGCA 1500  
 AAGAATTACA CATGAGGCTC CTCCGGCAGA AAATAGCCCA GCTGGAGGAG GAGAAGCAGG 1560  
 70 CACGCACGGC CTGGTGGTT GAGAGGGACA ACGCSCATCT TACCATCAGG AACTTGCAGA 1620  
 AGAAGGTGGA GAGGCTGCAG AAAGAGCTGA ACACGTGTCG AGACTTGCAC ACCGAGCTCA 1680  
 AAGCCAAACT GGCCGACACC AATGAACCTG AGATTAATAAC TTGGAACAG ACTAAAGCCA 1740  
 TTGAAGATCT AAACAAATCC AGAGACCAAC TGAAGAAGAT GAAGGAGAAA GCTGAGAAA 1800  
 AGCTCATGTC TGTCAGTGA GAACCTGGTA CCACAGAAAC TGAGGCTAAG GAGAAATAAG 1860  
 75 AAAGGGCCAG AAACATGATA GAAGTGGTAA CCAAGTAAAT GAAGACACTA AAAAAATCTC 1920  
 TGGGAAGAAG AGAAATGAGA GAAAGCAGC TGGCAGACT CAGGGAGGTG GTGTCGAGA 1980  
 TGCTAGGCTT GAACGTGACC AGCCTTGCTC TTCTTGATTA TGAATCATC AAGTGTCTTG 2040

AAAGATTGGT CCATTACAT CAGCATCACT TTGTTACCTG TGCTGCCTC AAAGATGTGA 2100  
 CTACTGGGCA AGAGAGGCAC CCACAAGGCC ATTTACAGCT TCTTCATTGA ACACGTGATC 2160  
 TCTTGAGAGA GGTGGCCATA AGACATGGCA CACAATTCOC AATTTACAA ATTCCCTCATG 2220  
 TCTTTGAGAT TTGATCAGIT TGTGAATATT TTATGCTTTG ATGATATAGT GAGAATGCAT 2280  
 5 CACTTGCAAA AACGATCTCA AAAGTGTGAG CCTTAGATAA ACGTCAGCAT TAAAAACGC 2340  
 CAAAAAAGC AAAAAAGC ATTTAGGAT CCAGAAGAAAT TCCACCAGAT TGCATGAGTT 2400  
 AGATTGGGAA ATGGGAGTGG GAGATAATAT TGGGAGGTAT CTATTTTAAG TCAGGGGCTT 2460  
 TACTAGCCGA TTTAGTTCTC ACAATAACCA TGTGGAGAAG CTGTGACATT TTTAATTAC 2520  
 10 AACCTTTCTG GGGCTCAGAC ATAAAGTTAC CTATCCAAGG TTGCAAGTTG GTAGTGGTGG 2580  
 GACCAGGATG GACAACCTAT TGGCCCTGCC TCAAAAGCCA TACCTCTTCT CCTGCTATGC 2640  
 AGAATCTGTT TCTCTGAAT CTCTGTGATG CTGGTGGGAA TTGTTTGCAT AGAGGAAGGA 2700  
 CAATAACCTT GCCATCGTGA GTTAATGTCC GGGCTGGTCA CAGTGGTTCA TGCTGTAAAT 2760  
 15 CCCAGCACTT TGGGAGTCCA AGGCAGGCAT ATCAATTGAG GTCAGGAGTT TAAGACCAGC 2820  
 CTGGCTAACA TAGTGAGACC CTGTTTCTAC TAAAAATACA AAAATAAGCC AGGTGTGGTG 2880  
 GTGCATGACT GTAATCCCA CTACTCAGCA GGAGAAGCAC TTGAACCCAG GAGACGGAGG 2940  
 CGGCAGTGAG CCAAGATTTGT GCCACTGCAC TCCAGCCTGG GCGACAGAGT GAAACTACAT 3000  
 CTCAGAAAAA AAAAAAAGC AAAAAAAGC AAGTTAATGT CCAAAAATGA CAGATTACA 3060  
 AGTGTAAGCT ATATGATTTT TCAAAAAGC AAAAGCAATA TACCTAATTC ATTTGGATCA 3120  
 20 AACTTACATA GGTCTCAGGT CCTGTAAGAA ACTTGCCTGT TCTAAGCTTT GCTACCAGAT 3180  
 TATATCTGGT GGTAAATGTT AATGTTTCAG CAGGGCTGGT CTCACTCTT TAAAAAGGAA 3240  
 AGCTTTATTT GGAGCCCAAC CCTATAAGAT GAAGAAATCC TATATAGTCT TATCACCA 3300  
 TATATCCAAT ACACCCACAG CAATGGTACC TTTTAAAGAT CAGGATTTTA TTATGAATTC 3360  
 CTGTCACTTT CTGTTTCCA TTTAAATTTT TATTTTACAA ATTTTTCAGG GAATCATATT 3420  
 25 CITTAACCTCA CTGAGAAAAA TGTGTTACTC TTTTGGACAA TTTATCTTAT TCTATCATA 3480  
 TAAGATGAT TTTTTATTG TCCTTAAAG AAGCTCTAGC ATGAAATTA AGGAAAGGGA 3540  
 AAGAAATAGA TCTGGTGCAC CCGAACATTA GGAGAAAATG AAAAAATAC AACCAACCGT 3600  
 TCGTGAGTCA TCAAAAAGC AAAGTCAGCC TGGCCAACAT GGCAAACTC CGTCTCTGCA 3660  
 AAAAAATACA AAATGAGCCC GGTATGTTGG CATATGCCTG TAATCCAGC TACTCGAGAG 3720  
 30 GCTGAGACAC GAAAAATGCT TGAACCTGGG AGCGGGAGGT TGAATGAGC CGAGATCGCG 3780  
 CTACTGCAC CTAGCTGGG CAACAGAGAG AGACCTTGTG TCAAAAACA ACAACAACA 3840  
 AAAGTCAAG TCATAATAAG CAAATTATTG GCTTCTTCT TCTAGACYAA AAGAAATTA 3900  
 AGAGATGAAA CAATCAATTG CAAGGGTCAA AACTAGATTG GATCTTGGTT TGAATGAAA 3960  
 AAAGCATAAA ATATCTTTC AATAATTGTA AAAATTGAA TGTGGACTAA GTCCTAGATT 4020  
 35 ATATTAAAT ATTTTAAAT TTTAAGCTT GACAAATGCA CTGATTGTTA TACTTAAAT 4080  
 AACTAAAAAT CTGAGATCC ACAGTGCTAC AGACAATAAA TGATAAATG GGAAAAA 4140  
 AAAAAAAAAA

Seq ID NO: 18 Protein sequence:

Protein Accession #: NP\_079335.1

1 11 21 31 41 51  
 MSLDCTSHIA LGAASPAPEE TYDHLSEVPV TREQLNHYRN VAQNARSELA ATLVPFECAQ 60  
 45 SELQDLRSKM LSKVSCQEL KAEMESYKEN NARKSSLLTS LRDRVQEELE ESAALSTSKI 120  
 RTEHTAHAAI KENQELKKKV VELNEKLQKC SKENBENKKQ VSKNCRKHHE FLTQLRDCLD 180  
 PDERNDKASD EDLILKLRDL RKENEFVKGQ IVILBETINV HEMEAASRE TMRLASEVN 240  
 REQKKAASCT EKKEKLNQDL LSAVEAKEAL EREVKIFQER LLAGQQVWDA SKQEVSLKK 300  
 50 SSSLEKSLK ASQDAVITSQ SQYSSPREKI AALLRGRLSM TGSTEDTILE KIREMDSREE 360  
 SRDRMVSQLE AQISELVEQL GKESGFHQKA LQRAQKAENM LETLQGQLTH LEALVSGGV 420  
 LRDNLNFEKQ KYLKFLDQLS QKMKLDQMAA ELGFDTRLDV VLARTEQLVR LESNAVLENK 480  
 TIAHNLQRKL KTQKERLESK ELHMSLLRQK IAQLEEEKQA RTALVVERDN AHLTIRNLQK 540  
 KVERLOKELN TCRDLHTELK AKLADTNELK IKTLBQTKAI EDLNRSDQL EKMKEKAEKK 600  
 55 LMSVKSELDI TEHEAKENKE RARNMIEVVT SEMKTLKKSLEBAEKREKQL ADFREVVSQM 660  
 LGLNVTSLAL PDYEIKCLE RLVHSHQHIF VTCACLKDV TQGERHPQGH LQLLH

Seq ID NO: 19 DNA sequence

Nucleic Acid Accession #: AF071552, NM\_000662

Coding sequence: 441-1313 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 65 CTTTGATATA GGCTCAGCTA AAAGGGAAT TGAGTGGGTC AGGTACCACG GATACTATAC 60  
 ACTCTATTGC ATGATTCTCC TGCCTACATC AGAAGACGTT TATAAGCCTA TTTAAAGGA 120  
 TACCAGTTGG AATCTCTCTT TTATTAATCA CCAAGAGAAC CATGAACAAG CTGTTTATCA 180  
 TTTGACTCAT CATTTAATCT TGATTTCAG CTCTCACAC TTGAAGAAG ACATAATACA 240  
 70 TTTCTCACAG GATTCTGGGA CTATTAACCT AACTATGTG TGTAAGAAGGA ATTCATACAA 300  
 TGAAAGCACT AGAAATAATT ATTATACTTA TAACCATTGT ATTTTACAT GTTTAAATA 360  
 TAGCCATAAT TAGCCTACTC AAATCCAAGT GTAAAAGTAA AATGATTGCT TTTGTTTTG 420  
 TTTCTCTGCG TTAGGGGATC ATGGACATTG AAGCATATCT TGAAAGAATT GGCTATAAGA 480  
 AGTCTAGGAA CAAATTGGAC TTGGAACAT TAACTGACAT TCTTCAACAC CAGATCCGAG 540  
 CTGTTCCCTT TGAGAACCTT AACATCCATT GTGGGGATGC CATGGACCTA GGCTTAGAGG 600  
 75 CCATTTTGA TCAAGTTGTG AGAAGAAATC GGGGTGGATG GTGTCTCCAG GTCAATCATC 660  
 TTCTGTACTG GGCTTGACC ACTATTGGTT TTGAGACCAC GATGTTGGGA GGGTATGTTT 720  
 ACAGCACTCC AGCCAAAAA TACAGCACTG GCATGATTCA CTTCTCTCTG CAGGTGACCA 780

TTGATGGCAG GAACTACATT GTCGATGCTG GGTTTGGACG CTCATACCAG ATGTGGCAGC 840  
 CTCTGGAGTT AATTCTGGG AAGGATCAGC CTCAGGTGCC TTGTGCTTC CGTTTGACGG 900  
 AAGAGAAATGG ATTCTGGTAT CTAGACCAAA TCAGAAGGGA ACAGTACATT CCAAATGAAG 960  
 AATTTCTTCA TTCTGATCTC CTAGAAGACA GCAAATACCG AAAAATCTAC TCCTTTACTC 1020  
 TTAAGCCTCG AACAAITGAA GATTTTGAAG CTATGAATAC ATACCTGCAG ACATCTCCAT 1080  
 CATCTGTGTT TACTAGTAAA TCATTTTGT CTTTGCAGAC CCCAGATGGG GTTCACTGTT 1140  
 TGGTGGGCTT CACCTCACC CATAGGAGAT TCAATTATAA GGACAATACA GATCTAATAG 1200  
 AGTTCAAGAC TCTGAGTGAG GAAGAAATAG AAAAAGTGCT GAAAATATA TTTAATATTT 1260  
 CCTTGCAGAG AAAGCTTGTG CCCAAACATG GTGATAGATT TTTTACTATT TAGAATAAGG 1320  
 AGTAAAAACA TCTTGTCTAT TTGTCATCCA GCTCACCAGT TATCAACTGA CGACCTATCA 1380  
 TGTATCTTCT GTACCCITAC CTATTTTGA AGAAAACTCT AGACATCAAA TCATTTACC 1440  
 TATAAAATG TCATCATATA TAATTAACA GCTTTTAAA GAAACATAAC CACAAACCTT 1500  
 TTCAAATAAT AATAATAATA ATAATAATA ATGTATTTA AAGATGGCCT GTGGTTATCT 1560  
 TGGAAATGG TGATTTATGC TAGAAAGCTT TTAATGTGG TTTATTGTTG AATTG

Seq ID NO: 20 Protein sequence:

Protein Accession #: NP\_000653.1

1 11 21 31 41 51  
 MDIEAYLERI GYKSKSRNKLD LETLTDILQH QIRAVPFENL NIHCGDAMD L GLEAIPDQVV 60  
 RRNRGGWCLQ VNHLLYWALT TIGFETMLG GYVYSTPAKK YSTGMHILL QVTIDGRNYI 120  
 VDAGFGRSYQ MWQPLELISG KDQPVPCVF RLTEENGFWY LDQIRREQYI PNEBFLHSDL 180  
 LEDSKYRKIY SFTLKRTIE DFESMNTYLQ TSPSSVFTSK SPCSQTIDG VHCLVGFITL 240  
 HRRPNYKNDT DLIEFKTLEB EIEKVLKNI FNISLQRKLV PKHGDRFFTI

Seq ID NO: 21 DNA sequence

Nucleic Acid Accession #:

NM\_003714

Coding sequence: 123-1031 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGGCACGAGC AAAAAGGAAG AGTGGGAGGA GGAGGGGAAG CGGCGAAGGA GGAAGAGGAG 60  
 GAGGAGGAAG AGGGGAGCAC AAAGGATCCA GGTCTCCCGA CGGGAGGTTA ATACCAAGAA 120  
 CCATGTGTGC CGAGCGGCTG GGCCAGTTCA TGACCTGGC TTTGGTGTG GCCACCTTTG 180  
 ACCCGGCGCG GGGGACCGAC GCCACCAACC CACCCGAGGG TCCCAAGAC AGGAGCTCCC 240  
 AGCAGAAAGG CCGCCTGTCC CTGCAGAATA CAGCGGAGAT CCAGCAGTGT TTGGTCAACG 300  
 CTGGCGATGT GGGGTGTGGC GTGTTTGAAT GTTTCGAGAA CAACCTCTGT GAGATTCGGG 360  
 GCTTACATGG GATTTGCATG ACTTTCTGC ACAACGCTGG AAAATTGTAT GCCCAGGGCA 420  
 AGTCATTCAT CAAAGACGCC TTGAATGTA AGGCCACGC TCTGCGGCAC AGGTTTCGGCT 480  
 GCATAAGCCG GAAGTGCCCG GCCATCAGGG AAATGGTGT CCAAGTTCAG CGGGAATGCT 540  
 ACCTCAAGCA CGACCTGTGC GCGGCTGCC AGGAGAACAC CCGGTGATA GTGGAGATGA 600  
 TCATTTCAA GGACTGTCTG CTGCACGAAC CCTACGTGGA CCTCGTGAAC TTGCTGTGTA 660  
 CCTGTGGGGA GGAGGTGAAG GAGGCCATCA CCCACAGCGT GCAGGTTTCA GTGAGCAGA 720  
 ACTGGGGAAG CCGTGTCTCC ATCTTGAGCT TCTGCACCTC GGCCATCCAG AAGCTCTCCA 780  
 CGGCGCCCCC CGAGCGCCAG CCCCAGGTGG ACAGAACCAA GCTCTCCAGG GCCCACCACG 840  
 GGGAAAGCAGG ACATCACCTC CCAGAGCCCA GCAGTAGGGA GACTGCGCGA GGTGCCAAGG 900  
 GTGAGCGAGG TAGCAAGAGC CACCACAAAC CCCATGCCG AGGCAGAGTC GGGGGCCTTG 960  
 GGGCTCAGGG ACCTTCCGGA AGCAGCGAGT GGGAAAGACA ACAGTCTGAG TATTCTGATA 1020  
 TCCGGAGGTG AATGAAAAGG CCTGGCCACG AAATCTTTC TCCACGCCGT CCAATTTCTT 1080  
 ATCTATGGAC ATTCAAAAC ATTTACCAT AGAGAGGGGG GATGTACAC GCAGGATTCT 1140  
 GTGGGACTG TGGACTTCAT CGAGGTGTGT GTTCGCGGAA CGGACAGGTG AGATGGAGAC 1200  
 CCTGGGGCC GTGGGTCTC AGGGTGCCT GGTGAATTCT GCACTTACAC GTACTCAAGG 1260  
 GAGCGCGCC GCGTTATCTT CGTACCTTTG TCTTCTTCC ATCTGTGGAG TCAGTGGGTG 1320  
 TCGGCGCTC TGTGTGGGG GAGGTGAACC AGGGAGGGG AGGGCAAGGC AGGGCCCCCA 1380  
 GAGCTGGGC ACACAGTGGG TGCTGGGCT CGCCCCGAAG CTTCTGGTGC AGCAGCCTCT 1440  
 GGTGCTGTCT CCGCGAAGT CAGGGCGGCT GGATTCCAGG ACAGGAGTGA ATGTAAAAAT 1500  
 AAATATCGCT TAGAATGCAG GAGAAGGGTG GAGAGGAGG AGGGCCGAG GGGGTGCTTG 1560  
 GTGCCAAACT GAAATTCAGT TTCTGTGTG GGGCCTTGG GTTCAGAGCT CTTGGCGAGG 1620  
 GTGGAGGGAG GAGTGTCAAT TCTATGTGTA ATTTCTGAGC CATGTACTG TCTGGGCTGG 1680  
 GGGGGCACT GTCCAAGGA GTGGCCCTTA TGAGTTTATA TTTTAACCAC TGCTTCAAAT 1740  
 CTCGATTTCA CTTTCTTAT TTATCCAGT ATATCTACAT ATCTGTATC TAAATAAATG 1800  
 GCTTCAAAAC AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 22 Protein sequence:

Protein Accession #: NP\_003705

1 11 21 31 41 51  
 MCAERLGQFM TLALVATFD PARGTDATNP PEGPQDRSSQ QKGRSLQNT AEIQHCLVNA 60  
 GDVGCQVFEC FENNSCEIRG LHGICMTFLH NAGKFDAGGK SFKIDALKCK AHALRHFRGC 120  
 ISRKCPAIRE MVSQLORECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180  
 CGEEVKEAIT HSVQVQCQBN WSLCSLSF CTSAIQKPPT APPRQPQVD RTKLSRAHHG 240  
 EAGHNLPEPS SRETGRGAKG ERGSKSHPNA HARGRVGGLG AQPSPGSEW EDEQSEYSID 300



RR

Seq ID NO: 23 DNA sequence

Nucleic Acid Accession #: NM\_005264.1

Coding sequence: 557-1954 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 10 | | | | |  
 GAATTCGGGC CAGAAAGAAAT CTGGCCTCGG AACACGCCAT TCTCCGCGCC GCTTCCAATA 60  
 ACCACTAACA TCCCTAACGA GCATCCGAGC CGAGGGCTCT GCTCGGAAAT CGTCCTGGCC 120  
 CAACTCGGCC CTTCGAGCTC TCGAAGATTA CCGCATCTAT TTTTITTTTC TTTTITTTCT 180  
 15 TTTCTAGCG CAGATAAAGT GAGCCCGGAA AGGGAAGGAG GGGCGGGGA CACCATTGCC 240  
 CTGAAAGAAT AAATAAGTAA ATAAACAAAC TGGCTCCTCG CGCAGCTGG ACGCGGTCGG 300  
 TTGAGTCCAG GTTGGGTCGG ACCTGAACCC CTAAAAGCGG AACCGCCTCC CGCCCTCGCC 360  
 ATCCCGGAGC TGAGTCGCGG GCGGCGGTGG CTGCTGCCAG ACCCGGAGTT TCCTCTTTCA 420  
 CTGGATGGAG CTGAAGCTTTG GCGGCGGAGA CCGCCTGGAT TGCCTGAAAG CCAGTGATCA 480  
 CTGAGCTCCC TCGGCAAGAC CCAGCGGCGG CTCGGGATTT TTTTGGGGGG GCGGGGACCA 540  
 20 GCCCGCGGCC GGCACCAIGT TCCTGGCGAC CCTGTACTTC GCGCTGCCGC TCTTGGACTT 600  
 GCTCCTGTGC GCCGAAGTGA GCGGCGGAGA CCGCCTGGAT TGCCTGAAAG CCAGTGATCA 660  
 GTGCTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCAGC CTAAGGCAGT GCGTGGCGGG 720  
 CAAGGAGACC AACTTCAGCC TGGCATCCGG CCTGGAGGCC AAGGATGAGT GCCGCAGCGC 780  
 CATGGAGGCC CTGAAGCAGA AGTCGCTCTA CAACTGCCGC TGAAGCGGG GTATGAAGAA 840  
 25 GGAGAAGAAC TGCCTGCGCA TTTACTGGAG CATGTACCA AGCCTGCAGG GAAATGATCT 900  
 GCTGGAGGAT TCCCATATG AACCAGTTAA CAGCAGATTG TCAGATATAT TCCGGGTGGT 960  
 CCCATTGATA TCAAGATGTT TTCAGCAAGT GGAGCACATT CCCAAAGGGA ACAACTGCCT 1020  
 GGATGCAGCG AAGGCTGCA ACCTCGACGA CATTGCAAG AAGTACAGGT CGGCCTACAT 1080  
 CACCCGCTGC ACCACGAGG TGTCCAACGA TGTCTGCAAC CGCCGCAAGT GCCACAAGGC 1140  
 30 CTTCCGGGAG TTTCTTGACA AGTTCGCCGC CAAGCACAGC TACGGAATGC TCTTCTGCTC 1200  
 CTGCCGGGAC ATCGCCTGCA CAGAGCGGAG GCGACAGACC ATCGTGCTGT TGTGCTCCTA 1260  
 TGAAGAGAGG GAGAAGCCCA ACTGTTTGAA TTTGCAGGAC TCCTGCAAGA CGAATTACAT 1320  
 CTGCAGATCT CGCCTTGGCG ATTTTITTTAC CAACIGCCAG CCAGAGTCAA GGTCTGTGAG 1380  
 CAGCTGTCTA AAGGAAAAC ACGCTGACTG CCTCCTCGCC TACTCGGGGC TTATTGGCAC 1440  
 35 AGTCATGACC CCCAATACCA TAGACTCCAG TAGCCTCAGT GTGGCCCCAT GGTGTGACTG 1500  
 CAGCAACAGT GGAACGAGC TAGAAGAGTG CTGAAATTT TTGAATTTCT TCAAGGACAA 1560  
 TACATGCTTT AAAAATGCAA TTCAAGCCTT TGGCAATGGC TCCGATGTGA CCGTGTGGCA 1620  
 GCCAGCCTTC CCAGTACAGA CCACCACTGC CACTACCACC ACTGCCCTCC GGGTTAAGAA 1680  
 CAAGCCCCTG GGGCCAGCAG GGTCTGAGAA TGAATTTCCC ACTCATGTTT TGCCACCGTG 1740  
 40 TGCAAAATTA CAGGCACAGA AGCTGAAATC CAATGTGTGC GGCAATACAC ACCTCTGTAT 1800  
 TTCCAATGGT AATTATGAAA AAGAAGGCTC CGGTGCTTCC AGCCACATAA CCACAAAATC 1860  
 AATGCTGTCT CTTCCAAGCT GTGCTCTGAG CCCACTGCTG GTCTGTGTGG TAACCGCTCT 1920  
 GTCCACCCTA TTATCTTAA CAGAAACATC ATAGCTGCAT TAAAAAATA CAATATGGAC 1980  
 ATGTAAAAAG ACAAAAACCA AGTTATCTGT TTCTGTCTT CTGTATAGC TGAATTTCCA 2040  
 45 GTTTAGGAGC TCAGTTGAGA AACAGTTCCA TTCAACTGGA ACATTTTIT TTTTCTTTT 2100  
 AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTGAAAAA CCGATGTCAG TGCTCCATCC 2160  
 AAACCTGAAA GGCCTTGGGA TAGCTGTAT TTAAAGGGA CAGTTTGTA CTGGGCTGT 2220  
 AAAGCAAAC TGGGCTGTGT TTTGATGAT GATGATCATC ATGATCATGA TGATTTTAAC 2280  
 AGTTTACTT CTGGCCTTTC CTAGTAGAG AAGGAGTTAA TATTCTAAG GTAACCTCCA 2340  
 50 TATCTCCTTT AATGACATTG ATTTCTAATG ATATAAATT CAGCCTACAT TGATGCCAAG 2400  
 CTTTITTTGCC ACAAAGAAGA TTCTTACCAA GAGTGGGCTT TGTGGAACA GCTGGTACTG 2460  
 ATGTTACCTT TTATATATGT ACTAGCATT TCCACGCTGA TGTATTGTA CTGTAACAG 2520  
 TCTGCACTT GTTACAAA GAAAAACCA CCCGGAATTC

Seq ID NO: 24 Protein sequence:

Protein Accession #: NP\_005255

1 11 21 31 41 51  
 60 | | | | |  
 MFLATLYFAL PLLDLLLSAE VSGGDRLCDV KASDQCLKEQ SCSTKYRTL RQCVAGKETNF 60  
 SLASGLEAKD ECRSAMEALK QKSLYNCRCK RGMKKEKNCL RIYWSMYQL QGNDLLEDSP 120  
 YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAKA CNLDDICKKY RSAIYTPCTT 180  
 SVSNDVCNRR KCHKALRQFF DKVPAKHSYG MLFCSCRDIA CTERRRQIV PVCSEYEEREK 240  
 65 PNCLNLQDSC KTNVYCRSL ADFFTNCQPE SRSVSSCLKE NYADCLLAYS GLIGTVMTPN 300  
 YIDSSLSVA PWDCDSNSGN DLEBCLKFLN FFKDNTCLKN AIQAFNGNSD VTVWQPAFPV 360  
 QTTTATTITTA LRKKNKPLGP AGSENEIPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY 420  
 EKEGLGASSH ITTKSMAAPP SCGLSPLLVL VVTALSTLLS LTETS

Seq ID NO: 25 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1576 (entire sequence represents open reading frame)

1 11 21 31 41 51  
 75 | | | | |  
 CTTTGTGTTT GCCATGCCTA GTCTAGTGGT ATCTGGAATA ATGGAAGAA ATGGGGGCTT 60  
 TGGAGAACTA GGATGTTTCG GGGGAAGCGC TAAGGACCGA GGGCTGCTGG AAGACGAGCG 120  
 CGCCCTTCAG CTGCTCTCG ATCAACTCTG CCTCCTGGGT TTGGGGGAGC CCCCCGCCCC 180

CAGGGCGGGG GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCCGCGCAGC CGACAGCCCC 240  
 CCCGAGCCGC GCGCCGCGCG CGCGCGCCGC GGGCGCCCGG GCGCGCCCGA CGACGGCCCC 300  
 CGCAGCGCAG ACGCCCCAGC CCCCCACCGC CCCCCAAGGG GCGAGCGACG CCAAGCTCTG 360  
 CGCTCTCTAC AAAGAGGCGG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT 420  
 5 TCCCTGTCCC ACCTCCGAGC ACCTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480  
 GGCCTTGAGG GCCAAGACCA ACACCTACAT CAAGACACCG GTGAGGGGCG AGGAACCACT 540  
 GTTCATGGTG ACAGGGGCGG GGGAGGACGT GGCCACAGCC CGGCGGGAAA TCATCTCAGC 600  
 AGCGGAGCAC TTCTCCATGA TCGTGCCTC CCGCAACAAG TCAGGCGCCG CCTTTGGTGT 660  
 GGCCTCTGCT CTGCCCCGCC AGGTGACCAT CCGTGTGCGG GTGCCCTACC GCGTGGTGGG 720  
 10 GCTGGTGGTG GGGCCCAAG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780  
 CATTATCACA CCAAGCCGTG ACCGCGACCC CGTGTTCGAG ATCAGGGGTG CCCCAGGCAA 840  
 CGTGGAGCGT GCGCGCAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900  
 CGAGTACAAC AATGAAAACG ACTTCTGGC GGGGAGCCCC GACGAGCAA TCGATAGCCG 960  
 CTACTCCGAC GCCTGGCGGG TGCACCAGCC CGGCTGCAAG CCCCTCTCCA CCTTCCGGCA 1020  
 15 GAACAGCCTG GGCTGCATCG GCGAGTGGG AGTGGACTCT GGTCTTGAGG CCCCAGCCT 1080  
 GGGTGAGCAG GCGGGGGACT TTGGCTACGG CGGTACCTC TTTCCGGGCT ATGGCGTGGG 1140  
 CAAGCAGGAT GTGTACTACG CGGTGGCCGA GACTAGCCCC CGGCTGTGGG CGGCGCAGGA 1200  
 GAAACGCCAG CCCACCTCCG TGCTTTCTC CTCTGCCCTC TCCTCTCTCT CCTCTCCGC 1260  
 CAAGGCCCCG GCTGGGCCCC CGGGGCGACA CGGCTCCCT GCCACTTCCG CGGAGCCCGA 1320  
 20 GCTGGCCGGA CTCCCGAGGC GCGCCCGGG AGAGCCGCTC CAGGGCTTCT CTAACCTTGG 1380  
 TGGGGCGGGC CTGCGGAGCC CCGGCGGGG GCGGGAATGC ATGGTCTGCT TTGAGAGCGA 1440  
 AGTGACTGCC GGCCTTGTGC CCTGCGGACA CAACCTGTTC TGCATGGAGT GTGCAGTACG 1500  
 CATCTGCGAG AGGACGGACC CAGAGTGTCC CGTCTGCCAC ATCAGAGCCA CGCAAGCCAT 1560  
 25 CCGAATATTC TCCTAA

Seq ID NO: 26 Protein sequence:

Protein Accession #: FGENESH predicted

30 1 11 21 31 41 51  
 FCFAMPSLVV SGIMERNNGGF GELGCFGGSA KDRGLLEDER ALQLALDQLC LLGLGEPPAP 60  
 RAGEDGGGGG GGAPAQPTAP PQPAPPPPA APPAAPTAP AAQTPQPPTA PKGASDAKLC 120  
 35 ALYKEAELRL KGSNTTECV PVPTSEHVAE IVGRQGCKIK ALRAKNTIYI KTPVRGEEPV 180  
 FMVTGREDV ATARREISA AEHFSMIRAS RNKSGAAGV APALPGQVTI RVRVPYRVVG 240  
 LVVGPKGATI KRIQQQNTY ITPSRDRDP VFEITGAPGN VERAREEIBT HIAVRTGKIL 300  
 EYNNENDFLA GSPDAIDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360  
 GEQGGDFGYG GYLFPYGVG KQDVVYVVAE TSPPLWAGQE NATPTSVLFS SASSSSSSA 420  
 40 KARAGPPGAH RSPATSAPE LAGLPKPPG EPLQGFSLKG GGLRSPGGG RDCMVCFESE 480  
 VTAALVPCGH NLFCECAVR ICERTDFECP VCHITATQAI RIFS

Seq ID NO: 27 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 ATGAGCGGTG CCGGGGTGGC GGCTGGGACG CCGCCCCCA GCTCGCCGAC CCCGGGCTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGCGA GAGCCCGCAG 120  
 50 CTCAGCGAGA GCGACCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAAACAAGG GTGAGCCGCG GCGGGGCCCT AGGCCGGCCC TGCTTCCCA GGCACACTCA 300  
 ACACGTCCCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360  
 55 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420  
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GCACAGATGC CGCTACCTCT 480  
 AGCCGTGGCT GACCATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGGAAGCCCA 540  
 GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660  
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCAGGCC CTATGGCTCT GAGTCTCAC 720  
 60 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGACAAA GGGAGGAAGC AGAGTCTTGT TTCCTTGCCA CTGTTCAGG 840  
 GCACITCCCC ATCCTGACAG CCGCCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020  
 65 GACATGAGA AGGGGTTGA GGGAGGGCCC TTCCCTAGCC GTGTGGCAA CTCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCAAGTCCG CAGCCCCAGC CTGCACTGC TGGGAGCGCT 1140  
 GACAGGACAC GGAAGAGGC CATGCTTCC CTGCGGACCT GCTGTCCAT GTGTCCAA 1200  
 CCTCTGCT TTCCAGATT CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTG 1260  
 GCGCTGCT GGGTCTGCAT CAACGAGGTG TGGGTAGAGC CCGGAGGACC CAGCCCTGCC 1320  
 70 AGGCTGAAGG AGGCTCTCT ACAGACACAC AGGCCAGGAG GCAAGCGTGG GGTCTTGGC 1380  
 GGCGGTAGCG CCGACACTGT GCGCTCTCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATT AAAAGCTGAC GTCTCCAGA AGCGGACCT GGAAGAGGAG 1560  
 75 CCCCTACTT ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGGCA GGCCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680  
 AGGCAGATGG GGGCGGGG ACACCCCCA ATGATCTTGC CCCTTCCCT GCGAAAGCCC 1740  
 ACCACACTTA GGCAGTGCA AGTGCTCATC CCGAGCTGT GGAATACCAA CCTCTCGAC 1800

ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860  
 CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
 CTGAAGCAGA CCCCGAAGAA CAACCTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040  
 AAACGGCGCC TGCATCGCTC AGTGCTTGA

Seq ID NO: 28 Protein sequence:

Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 MSGAGVAAAG RPPSSPTPGS RRRQRPSVG VQSLRQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPPQAH S TLPLQHRNT AINSSTR LGS 120  
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSPMALSPH 240  
 MLGAQGIWTH SIQGSIPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSGPH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVEGGP FFSRCGNSSE 360  
 LFWAKCGPSR PQPQCSAGDA DRTREEAMLS LGTCCSMCPK PSCFPDPSG NHLRSASAPL 420  
 GARWVCINGV WVEPGGSPSA RLKEGSSRTH RFGGKRGR LA GGSADTVRSP ADSLSMSSFP 480  
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGGQARK 540  
 EKAASNAGA ACMGNSQHQG RQMGA GAHP MLLPLRKP TTLRQCEVLI RELWNTNLLQ 600  
 TQELRLKSL LEGSQRPQA PEEASFPRDQ BATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNFPA ERQKRLQAMQ KRLHRSVL

Seq ID NO: 29 DNA sequence

Nucleic Acid Accession #:

NM\_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCGTGCCGA ATTCGCGCAG AGACCGCGTG TTGCGCCTG GTAGAGATT CTCGAAGACA 60  
 CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC 120  
 GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTGTGCTCTG ACCTTTGCC 180  
 TCTCTGTAC AAATCCCCTT CATGAAC TAA AGCAGCTGC TTTCCCCCAG ACCACTGAGA 240  
 AAATTAGTCC GAATTGGGAA TCTGGCATT A TGTTGACTT GGCAATTTCC ACACGGCAAT 300  
 ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCITTTGTA GTTGAAGGGT 360  
 TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAAITCCAT ATACACCATG 420  
 ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTAC TCAGACCATG 480  
 AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540  
 CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTTCA 600  
 GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACC ACCAGAACAT GCCAGTGGTA 660  
 GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720  
 TCTCTGAAGG AACTCACTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTTCC 780  
 CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAAGAGCCGG GTGAGCCGGC 840  
 GAAAACAAAA TGAATAATCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960  
 GCATGGGCAT CAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020  
 TCAACCAAAAT TGATGCTAGA TCTTGCTGA TCCATACAAG TGAAGAAGAG GCTGAAATCC 1080  
 CTCCAAAGAC CTATTCTAT CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCATCA 1140  
 TCAGTTCTCT GTCTCTGCTG GGGGTTATCT TAGTGCTCT CATGAATCGG GTGTTTTTCA 1200  
 AATTCTCTCT GAGTTTCTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260  
 TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320  
 CAATGGAAAT GAAAGAGAGA CCACCTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380  
 GTGCCATTTT TGATTCCACG TGAAGGGTC TAACAGCTCT AGGAGGCCCTG TATTTCATGT 1440  
 TTCTGTGTA ACATGTCTCT ACATTGATCA AACAATTAA AGATAAGAAG AAAAAGAATC 1500  
 AGAAGAAACC TGAATAATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT 1560  
 CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTC 1620  
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 AAGAGGTTCAT GATAGTTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740  
 GGTGCAAGAA TAAATGCCAT TCACATTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800  
 TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACACCATC 1860  
 CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT 1920  
 TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGGC CTAGCAATTG 1980  
 GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC 2040  
 ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100  
 AGCAGGCTGT CCTTTATAAT GCATTGTGAG CCATGCTGGC GTATCTTGGG ATGGAACAG 2160  
 GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTTCGA CTACTGCTG 2220  
 GCTTATTCAT GTATGTTGCT CTGTTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280  
 GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340  
 GTTTTGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC CGTATAAATT 2400  
 TCTAGTTAAG GTTTAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460  
 AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGG TTTGTGATT 2520  
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 AAAAAACACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAAG TATAAAAAGG 2940  
 CAGAATTAGT ATAGAGTACA TTCATTAAC ATTTTGTCA GGATTATTC CCGTAAAAAC 3000  
 GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTGTATAAT ACAGAAATCT 3060  
 AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120  
 TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGIT TATGTATCAC CAGACTGGGT 3180  
 TATTGCCAAG TTATATATCA CCAAAGCTG TATGACTGGA TGTCTGGTT ACCTGGTTTA 3240  
 CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAANAAT AACTAAAGTA 3300  
 TCATTGATT CGATTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCAATTGT 3360  
 GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420  
 GATGTTCTTT TTTTACCAA TAAATTCCTT ATATCAGCTT G

Seq ID NO: 30 Protein sequence:  
 Protein Accession #: NP\_036451.2

1 11 21 31 41 51  
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 MARKLSVILI LTFALSVNTP LHELKAAAF QTTEKISPNW ESGINVDLAI STROYHLQQL 60  
 FYRYGENNSL SVEGRKLLQ NIGIDKIKRI HHHHDDHHS DHEHSDHER HSDHEHSDH 120  
 EHHSDHHS HENHAAAGKN KRKALCPDHD SDSSGKDPN SQKGHAHRPE HASGRNVKD 180  
 SVSASEVTST VYNTVSEGTH FLETITPRP GKLFKDVSS STPPSVTSKS RVSRLAGRKT 240  
 NESVSEPRKG FMYSRNTNEN PQECFNASKL LTHSGMGIOV PLNATEFNYL CPAIINQDA 300  
 RSLIHTSEK KAEIPKTYL LQIAWVGFI AJSHISL LGLVILVPLMN RVFFKFLSLF 360  
 LVALAVGTLS GDAFLHLLPH SHASHHSHS HEEPAMEMKR GLFSLHSSQ NIEESAYFDS 420  
 TWKGLTALGG LYFMFLVHV LTLKQFKDK KKKNQKPPEN DDDVEKKQL SKYESQLSTN 480  
 EEKVDTDRT EGYLRADSQE PSFSDSQPA VLEEEVVMIA HAHPOEVYNE YVPRGCKNKC 540  
 HSHFHDITLGQ SDDLHHHHH YHHLHHHH QNHHPHSHS RYSREELKDA GVATLAWMVI 600  
 MGDGLHNSFD GLAIGAAFTG GLSSGLSTV AVFCHLPHE LGDFAVLLKA GMTVKQAVLY 660  
 NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720  
 RWGYFFLQNA GMLLGFIML LISIFHKIV FRINF

Seq ID NO: 31 DNA sequence  
 Nucleic Acid Accession #: NM\_002184.1  
 Coding sequence: 256-3012 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 GAGCAGCAA AAGGCCCGCG GAGTCGCGCT GGGCCGCCCC GGCGCAGCTG AACCGGGGGC 60  
 CGCGCTGCC AGGCCGACGG GTCTGGCCCA GCCTGGCCCG AAGGGGTTCC TCGCTGTGG 120  
 AGACGGGAG GGTGCGAGCG GCGCGGCCCT AGTGAAACCC AATGGAAAAA GCATGACATT 180  
 TAGAAGTAGA AGACTTAGCT TCAATCCCT ACTCCTTAC TACTAATTT TGTGATTGG 240  
 AAATATCCGC GCAAGATGTT GACGTTGCG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC 300  
 CTCACCACTG AATCTACAGG TGAACCTCTA GATCCATGTG GTTATATCAG TCCTGAACTC 360  
 CCAGTTGTAC AACTTCATTC TAATTTCACT GCAGTTTGTG TGCTAAAGGA AAAATGTATG 420  
 GATTATTTTC ATGATAATGC TAATTACATT GTCTGGAAAA CAACCAATT TACTATTCTT 480  
 AAGGAGCAAT ATACTCAT ATACAGAAAC GCATCCAGTG TCACCTTTAC AGATATAGCT 540  
 TCATTAAATA TTCAGCTCAC TTGCAACATT CTACATTCG GACAGCTTGA ACAGAAATGT 600  
 TATGGAATCA CAATAATTTC AGGCITGCCCT CCAGAAAAAC CTAAAAATT GAGTTGCATT 660  
 GTGAACGAGG GGAAGAAAAAT GAGGTGTGAG TGGGATGGTG GAAGGGAAAC ACACCTGGAG 720  
 ACAAACTTCA CTTAAAAATC TGAATGGGCA ACACACAAGT TTGCTGATTG CAAAGCAAAA 780  
 CGTGACACCC CCACCTCATG CACTGTTGAT TATCTACTG TGTATTTGT CAACATTGAA 840  
 GTCTGGGTAG AAGCAGAGAA TGCCCTTGGG AAGGTTACAT CAGATCATAT CAATTTTGTG 900  
 CCTGTATATA AAGTGAAGCC CAATCCGCCA CATAATTTAT CAGTGATCAA CTCAGAGGAA 960  
 CTGCTAGTA TCITAAATTT GACATGGACC AACCCAAGTA TTAAGAGTGT TATAATACTA 1020  
 AAATATAACA TTCAATATAG GACCAAAGAT GCCTCAACTT GGAGCCAGAT TCCTCCTGAA 1080  
 GACACAGCAT CCACCGCATC TTCATTCAT GTCCAAGACC TTAACCTTT TACAGAATAT 1140  
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 GAAGCAAGTG GGATCACCTA TGAAGATAGA CCATCTAAAG CACCAAGTTT CTGGTATAAA 1260  
 ATAGATCCAT CCCATACTCA AGGCTACAGA ACTGTACAAC TCGTGTGGAA GACATTCCTT 1320  
 CCTTTGAAG CCAATGGAAA AATCTTGGAT TATGAAGTGA CTCTCACAAG ATGGAAATCA 1380  
 CATTTACAAA ATTACACAGT TAATGCCACA AAACGTGACG TAAATCTCAC AATGATCGC 1440  
 TATCTAGCAA CCTAACAGT AAGAAATCTT GTTGGCAAAT CAGATGCAGC TGTTTTAACT 1500  
 ATCCCTGCCCT GTGACTTTCA AGCTACTCAC CCTGTAATGG ATCTTAAAGC ATTCCTCAAA 1560  
 GATAACATGC TTTGGGTGGA ATGGACTACT CCAAGGGAAT CTGTAAGAAA ATATATACTT 1620  
 GAGTGGTGTG TGTATCAGA TAAAGCACCC TGTATCACAG ACTGGCAACA AGAAGATGGT 1680  
 ACCGTGCATC GCACCTATT TAAAGGGGAA TTAGCAGAGA GCAAAATGCTA TTTGATAACA 1740  
 GTTACTCCAG TATATGCTGA TGGACCAGGA AGCCCTGAAT CCATAAAGGC ATACCTTAAA 1800  
 CAAGCTCCAC CTTCAAAGG ACCTACTGTT CGGACAAAAA AAGTAGGGAA AACCGAAGCT 1860  
 GTCTTAGAGT GGGACCAACT CCTGTTGAT GTTCAGAAAT GATTATCAG AAATTTAACT 1920  
 ATATTTTATA GAACCATCAT TGGAAATGAA ACTGCTGTGA ATGTGGATT TCCACACA 1980  
 GAATATACAT TGTCTCTTT GACTAGTGAC ACATTGTACA TGGTACGAAT GGCAGCATAC 2040  
 ACAGATGAAG GTGGGAAGGA TGGTCCAGAA TTCACCTTTA CTACCCCAAA GTTTGCTCAA 2100  
 GGAGAAATTG AAGCCATAGT CTGCGCTGTT TGCTTAGCAT TCCTATTGAC AACTCTTCTG 2160  
 GGAGTGCTGT TCTGCTTTAA TAAGCGAGAC CTAATTAATA AACACATCTG GCCTAATGTT 2220  
 CCAGATCCTT CAAAGAGTCA TATTGCCAG TGTCCACCTC ACCTCTCTCC AAGGCACAA 2280

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 ACTGTCCAGT ATTCTACCGT GGTACACAGT GGCTACAGAC ACCAAGTTCC GTCAGTCCAA 2580  
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 CTACAATTAG TAGATCATGT AGATGGCGGT GATGGTATTT TCCCCAGGCA ACAGTACTTC 2700  
 AAACAGAACT GCAGTCAGCA TGAATCCAGT CCAGATATTT CACATTTTGA AAGGTCAAAG 2760  
 CAAGTTTCAT CAGTCAATGA GGAAGATTTT GTTAGACITTA AACAGCAGAT TTCAGATCAT 2820  
 ATTTCAAAAT CCGTGGGATC TGGGCAAAATG AAAATGTTTC AGGAAGTTTC TGCAGCAGAT 2880  
 GCITTTGGTC CAGGTACTGA GGGACAAGTA GAAAGATTG AAACAGTTGG CATGGAGGCT 2940  
 GCGAGTATG AAGGCATGCC TAAAAGTTAC TTACCACAGA CTGTACGGCA AGGCGGCTAC 3000  
 ATGCCTCAGT GAAGGACTAG TAGTCTCTGC TACAACITCA GCAGTACCTA TAAAGTAAAG 3060  
 CTAATAATGAT TTTATCTGTG AATTC

Seq ID NO: 32 Protein sequence:

Protein Accession #: NP\_002175.1

1 11 21 31 41 51  
 MLTLQTVVWQ ALFILTTS TELLDPGCGY ISPESPVVQL HSNFTAVCVL KEKCMDYFHV 60  
 NANYVWKTN HFTIPKEQYT IINRTASSVT FTDIASLNIQ LTCNLTFGQ LEQNVYGIIT 120  
 ISGLPFEKPK NLSCIVNEGK KMRCEWDGGR ETHLENTFL KSEWATHKFA DCKAKRDPT 180  
 SCTVDYSTVY FVNIEVWVEA ENALGKVTSD HINFDPVYKV KPNPPHNLV INSEELSSIL 240  
 KLTWTNPSK SVILKYNQY YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300  
 CMKEDGKGYW SDWSEASGI TYEDRPSKAP SFWYKIDPSH TQGYRTVQLV WKILPFEAN 360  
 GKILDYEVTL TRWKSILQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420  
 FQATHPVMDL KAFPKDNMLW VEWITPRESV KKYILEWCVL SDKAPCIDW QQEDGTVHRT 480  
 YLRGNLAESK CYLITVTPVY ADGPGSPESI KAYLKQAPPS KGPTVRTKKV GKNEAVLEWD 540  
 QLPVDVQNGF IRNYTIFYRT HGNETAVNV DSSHTYITLS SLTSDILYMV RMAAYTDHGG 600  
 KDGPFTFTT PKFAQGEIEA IVPVCLAF LTTLLGVLF FNRDLIKKH IWPVNPDPK 660  
 SHIAQWSPHT PPRHNFNSKD QMYSDFNFTD VSVVEIEAND KKPPEDLKS LDLFKKEKIN 720  
 TEGHSSGIGG SSCMSSSRPS ISSDENESS QNTSSTVQYS TVVHSGYRHQ VPSVQVFSRS 780  
 ESTQPLLDSE ERPEDLQLVD HVDGGDGILP RQQYFKQNC QHSSPDISH FERSKQVSSV 840  
 NEEDFVRLKQ QSDHISQSC GSGQMKMPQE VSAADAFPG TEGQVERFET VGMEAATDEG 900  
 MPKSYLPQTV RGGGYMPQ

Seq ID NO: 33 DNA sequence

Nucleic Acid Accession #: NM\_018255.1

Coding sequence: 11-2491 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 AGTGGCGGAC ATGGTGGCAC CCGTGCTGGA GACTTCTCAC GTGTTTGTCT GCCCAAACCG 60  
 GGTGCGGGGA GTCTGAACT GGAGCTCTGG GCCCAGAGGA CTCTGGCCT TTGGCACGTC 120  
 CTGCTCCGTG GTGCTCTATG ACCCCCTGAA AAGGGTGTGT GTTACCAACT TGAATGGTCA 180  
 CACCGCCCGA GTCAATTGCA TACAGTGGAT TTGTAAACAG GATGGCTCCC CTCTACTGA 240  
 ATTAGTTTCT GGAGGATCTG ATAATCAAGT GATCACTGG GAAATAGAGG ATAATCAGCT 300  
 TTTAAAGGCA GTGCATCTTC AAGGCCATGA AGGACCTGTT TATGCGGTGC ATGCTGTTTA 360  
 CCAGAGGAGG ACATCAGATC CTGCATTATG TACACTGATC GTTCTGCAG CTGCAGATTC 420  
 TGCTGTTCGA CTCTGGTCTA AAAAGGGTCC AGAAGTAATG TGCCTTCAGA CTTTAAACTT 480  
 TGGAAATGGA TTTGCTTTGG CTCTCTGCTT ATCTTTTITG CCAATACCTG ATGTACCAAT 540  
 ATTAGCATGT GGCAATGATG ATTGCAGAA TACATATTT GCTCAACAAA ATGATCAGTT 600  
 TCAGAAAGTG CTCTCTCTCT GTGGACATGA GGATTGGATT AGAGGAGTGG AATGGGCAGC 660  
 CTTTGGTAGA GATCTTTTCC TAGCAAGCTG TTCACAAGAT TGCTGATAA GAATATGGAA 720  
 GCTGTATATA AAGTCAACAT CTTTAGAAAC TCAGGATGAC GATAACATAA GACTGAAAGA 780  
 AAATACTTTT ACCATAGAAA ATGAAAGTGT TAAAATAGCA TTGCTGTTA CTCTGGAGAC 840  
 AGTGCTAGCC GGTCAAGAAA ACTGGGTAAA TGCAGTTCAC TGGCAACCTG TGTTTTACAA 900  
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 AGGTGGGAAT ACTTTGGGAT TTTATGATTG CCAGTTCAAT GAAGATGGCT CCATGATCAT 1080  
 TGCTCATGCT TTCCACGGAG CGTTGCACCT TTGGAAACAG AATACAGTTA ACCCAAGAGA 1140  
 GTGGACTCCA GAGATTGTCA TTTCAAGACA CTTTGATGGT GTCCAAGACC TAGTCTGGGA 1200  
 TCCAGAAGGA GAATTATTA TCACTGTGG TACTGATCAG ACACTAGAC TTTTGTCTCC 1260  
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 TGAAAAAGTT CTGCGGTTT TTCTGCACC TCGGAAITTT GTGGAAAAIT TTTGTGCCAT 1440  
 TACAGGACAA TCACTGAATC ATGTGCTCTG TAATCAAGAT AGTGATCTTC CAGAAGGAGC 1500  
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 GCTTCTGAT GAACAGGAGC TGTAACTAG TACTGGTTT GAGTATCAGC AGGTGGCCTT 1620  
 TCAGCCCTCC ATACTTACTG AGCCTCCAC TGAGGATCAT CTCTGCAGA ATACTTGTG 1680  
 GCTGAAGT CAAAACTAT ATGGGCACGG TTATGAAATA TTTTGTGTTA CTGTGAACAG 1740  
 TTCAAAGACT CTGCTGCTT CAGCTGTGTA GGCAGCTAAG AAAGAGCATG CAGCTATCAT 1800  
 TCTTTGGAAC ACTACATCTT GGAACAGGT GCAGAATTTA GTTTCCACA GTTTGACAGT 1860  
 CACGCAGATG GCCTTCTCAC CTAATGAGAA GTTCTTACTA GCTGTTTCCA GAGATCGAAC 1920  
 CTGGTCATTG TGGAAAAAGC AGGATACAAT CTCACCTGAG TTCAGGCCAG TTTTGTGCT 1980  
 TTTTGCCTTC ACCAACAATA TACTTCTGT GCACAGTAGA ATTATTTGGT CTGTGATTG 2040

GAGTCTGAC AGCAAGTATT TCTTCACTGG GAGTCGAGAC AAAAAAGTGG TTGTCTGGGG 2100  
 TGAGTGGCAG TCCACTGATG ACTGTATTGA GCACAACATT GGGCCCTGCT CCTCAGTCCT 2150  
 GGACGTGGGT GGGGCTGTGA CAGCTGTGAG CGTCTGCCCA GTGCTCCACC CTCTCAACG 2220  
 ATACGTGGTT GCAGTAGGAT TGGAGTGTGG AAAGATTTGC TTATATACCT GGAAGCAAGAC 2280  
 TGATCAAGTT CCAGAAATAA ATGACTGGAC CCACTGTGTA GAAACAAGTC AAAGCCAAAG 2340  
 TCATACACTG GCTATCAGAA AATTATGCTG GAAGAATTGC AGTGGAAAAA CTGAACAGAA 2400  
 GGAAGCAGAA GGTGCTGAGT GGTACACTT TGCAAGCTGT GGTGAAGATC ACACGTGTGA 2460  
 GATACACAGA GTCATAAAT GTGCACTGTA ATGG

Seq ID NO: 34 Protein sequence:  
 Protein Accession #: NP\_060725.1

1 11 21 31 41 51  
 MVAPVLETSV VFCCPNRVRG VLNWSSGPRG LLAFGTSCSV VLYDPLKRVV VTNLNGHTAR 60  
 VNCIQWICKQ DGSFSTELVS GGSNDQVIHW EIEDNQLLKA VHLQGHGEPV YAVHAVYQRR 120  
 TSDPALCTLI VSAAADSAVR LWSKKGPPEVM CLQTLNFGNG FALALCLSL PNTDVPILAC 180  
 GNDDCRIHF AQNDQFQKV LSLCGHEDWI RGVWAAFGF DLFLASCSQD CLIRIWKLYI 240  
 KSTSLETQDD DNIRLKENTF TIENESVKIA FAVILETVLA GHENWVNAVH WQPVFYKDG 300  
 LQQPVRLLSA SMDKTMILWA PDESGVWLE QVRVGEVGGN TLGFYDCQFN EDGSMJIAHA 360  
 FHGALHLWKQ NTVNPREWTP EIVISGHFDG VQDLVWDPEG EFITVGTDO TTRLFAPWKR 420  
 KDQSQVTHIE IARPOJHGYD LKCLAMINRF QFVSGADEKV LRVFSAPRNF VENFCAITGQ 480  
 SLNHVLCNQG SDLPFGATVP ALGLSNKAVF QGDIASQPSD EELLTSTGF EYQVAFQPS 540  
 ILTEPTEDH LLQNTLWPBV QKLYGHGYEI FCVTCNSSKT LLASACKAAK KEHAAHLWN 600  
 TTSWKQVQNL VFHSLTVTQM AFSNPKFLL AVSRDRTWSL WKKQDTISPE FEPVFSLPF 660  
 TNKITSVHSR IHSWCDWSPD SKYFFTGSRD KKVYVWGECD STDDCIEHNI GPCSSVLDVG 720  
 GAVTAVSVCP VLHPSQRYVV AVGLECGKIC LYTWKKTQV PEINDWTHCV ETSQSQSHL 780  
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Seq ID NO: 35 DNA sequence  
 Nucleic Acid Accession #: NM\_022131  
 Coding sequence: 11-2878 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 TGCTGCGAGG ATGCTGCGCTG GCGGCGCTGTG CTGGGTGCGG CTCTGCTGG CGCTGGGCGT 60  
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 CAATAAGCAC AAGCCATGGA TCGAGACTTC ATATCATGGA GTCATACTG AGAACATGA 180  
 CACAGTCATT TTGGACCCAC CACTGGTAGC CCTGGATAAA GATGCACCGG TTCTTTTTC 240  
 AGGGGAAATC TGTGCGTTCA AGATCCATGG CCAGGAGCTG CCCTTTGAGG CTGTGGTGCT 300  
 CAACAAGACA TCAGGAGAGG GCCGGCTCCG TGCCAAGAGC CCCATTGACT GTGAGTTGCA 360  
 GAAGGAGTAC ACATTTCATC TCCAGGCCTA TGACTGTGGT GCTGGGCCCC ACGAGACAGC 420  
 CTGGAAAAAG TCACACAAGG CCGTGGTCCA TATACAGGTG AAGGATGTCA ACGAGTTTGC 480  
 TCCACCTTC AAAGAGCCAG CTACAAGGC TGTGTGACG GAGGGCAAGA TCTATGACAG 540  
 CATTCTGCAG GTGGAGGCCA TTGACGAGGA CTGCTCCCCA CAGTACAGCC AGATCTGCAA 600  
 CTATGAAATC CTCACACAG ATGTGCCTTT TGCCATCGAC AGAAATGGCA ACATCAGGAA 660  
 CACTGAGAA GTAGCTATG ACAACAACA CCAGTATGAG ATCCTGGTGA CCGCCTACGA 720  
 CTGTGGACAG AAGCCCGCTG CTCAGGACAC CCTGGTGCAG GTGGATGTGA AGCCAGTTTG 780  
 CAAGCCTGGC TGCCAAGATC AGACCAAGAG GATTGAGTAC CAGCCTGGCT CCGGGAGCAT 840  
 GCCCTGTTC CCGAGCATCC CCTGGAGAC GTGCGATGGA GCGGTGTCTT CCCTCCAGAT 900  
 CGTCACAGAG CTCGAGACTA ATTACATTGG GAAGGGTTGT GACCGGGAGA CCTACTCTGA 960  
 GAAATCCCTT CAGAAGTTAT GTGGAGCCTC CTCTGGCATC ATTGACCTCT TGCCATCCCC 1020  
 TAGCGTGCC ACCAATGGA CTGCAAGACT GCTGGTGGAC AGCAGTGAGA TGATCTTCAA 1080  
 GTTTGACGGC AGGCAGGGTG CAAAATCCC CGATGGGATT GTGCCAAGA ACCTGACCGA 1140  
 TCAGTTCAAC ATCACCATGT GGATGAAACA CGGCCCCAGC CCTGGTGTGA GAGCCGAGAA 1200  
 GGAACCATC CTCTGCAACT CAGACAAAAC CGAAATGAAC CCGCATCACT ATGCCCTGTA 1260  
 TGTGCACAAC TGCCGCTCG TCTTTCTCTT GCGGAAGGAC TTCGACCAGG CTGACACCTT 1320  
 TCGCCCCGCG GAGTTCCACT GGAAGCTGGA TCAGATTGTG GACAAAGAGT GGCCTACTA 1380  
 TGTCACTAAT GTGGAGTTTC CTGTGGTAAC CTTATACATG GATGGAGCAA CATATGAACC 1440  
 ATACCTGGTG ACCAACGACT GGCCCATTC ATCATCTCAC ATAGCCATGC AACTCAGAGT 1500  
 CGGCGCTTGT TGCCAAGGAG GAGAAGTCAC CAAACCACAG TTTGCTCAGT TCTTTCATGG 1560  
 AAGCTGGCC AGTCTACCA TCCGCCCTGG CAAAATGGAA AGCCAGAAGG TGATCTCCTG 1620  
 CCTGCAGGCC TGCAAGGAAG GGCTGGACAT TAATCCTTG GAAAGCCTTG GCCAAGGAAT 1680  
 AAAGTATCAC TTCAACCCCT CGCAGTCCAT CTTGGTGATG GAAGGTGACG ACATTGGGAA 1740  
 CATTAAACCGT GCTCTCCAGA AAGTCTCCTA CATCAACTCC AGGCAGTTCC CAACGGCGGG 1800  
 TGTGCGGCGC CTCAAAGTAT CCTCCAAAGT CCAGTGCTTT GGGGAAGACG TATGCATCAG 1860  
 TATCCCTGAG GTAGATGCCT ATGTGATGGT CCTCCAGGCC ATCGAGCCCC GGATCACCTT 1920  
 CCGGGGCACA GACCACCTTC GGAGACCTGC TGCCCAAGTT GAAAGTGCCA GGGGAGTGAC 1980  
 CCTCTTCCCT GATATCAAGA TTGTGAGCAC CTTCGCCAAA ACCGAAGCCC CCGGGGACGT 2040  
 TGACATTTG GTGATCGGAG GGGACTTGGG CCAAGGCCAG GAGTGCITGG AGCTCAACCA 2100  
 CAGTGAGCTC CACCAACGAC ACCTGGATGC CACTAATTCT ACTGCAGGCT ACTCCATCTA 2160  
 CGGTGTGGGC TCCATGAGCC GCTATGAGCA GGTGCTACAT CACATCCGCT ACCGCAACTG 2220  
 GCGTCCGGCT TCCCTGAGG CCGGGCGTTT CCGGATTAAG TGCTCAGAAC TCAATGGGCG 2280  
 CTACACTAGC AATGAGTTCA ACTTGGAGGT CAGCATCCTT CATGAAGACC AAGTCTCAGA 2340  
 TAAGGAGCAT GTCAATCATG TGATTGTGCA GCCTCCCTTC TCCAGTCTG TCCATCATCC 2400  
 TGAGTCCCGG AGTAGCATCC AGCACAGTTC AGTGGTCCCA AGCATTGCCA CAGTGGTCAT 2460

CATCATCTCC GTGTGCATGC TTGTGTTTGT CGTGGCCATG GGTGTGTACC GGGTCCGGAT 2580  
 CGCCCCACCAG CACTTCATCC AGGAGACTGA GCCTGCCAAG GAATCTGAGA TGGACTGGGA 2640  
 CGATTCTGCG CTGACTATCA CAGTCAACCC CATGGAGAAA CATGAAGGAC CAGGGCATGG 2700  
 GGAAGATGAG ACTGAGGGAG AAGAGGAGGA AGAAGCCGAG GAAGAAATGA GCTCCAGCAG 2760  
 TGGCTCTGAC GACAGCGAAG AGGAGGAGGA GGAGGAAGGG ATGGGCAGAG GCAGACATGG 2820  
 GCAGAAATGGA GCCAGGCAAG CCCAGCTGGA GTGGGATGAC TCCACCCTCC CCTACTAGTG 2880  
 CCCAGGGGTC TGCTGCCTGG CCCACATGTC CCTTTTGTA ACCCTGACCC AGTGTATGCC 2940  
 CATGTCTATC ATACCTCACC TCTGATGTCT GTGACATGTC TGGGAAGGCC TTCTCCAGCT 3000  
 TCCTGGAGCC CACCCTTTAA GCCTTGGGCA CTCCTGTGT TTCATCCATG GGAAGTTC 3060  
 AAGAAGCCCA GCATGGCCAT CAGTGAGGAC TTCAGGGTAG ACTTTGTCT GTAGCCTCCA 3120  
 CTCTGCCCT AAGTTCCCA GCATCCTGAC TACCTGTCTG CAGAGTTTC CTTTGTTTT 3180  
 TCCTGCAGG AAGAAGGCC ACCTTTGTGT CACTCACCTC CCCAGGCTCA GAGTCCCAA 3240  
 GGCCCTGGGG TTCCAACCTA CTGTGCGTCT CCTCCACACA GACCAAGTAG TTCTCCTATG 3300  
 CTGACTCCAG GTTGCTTCAT ACAAGGAGGG TGGTTGAAGT TCACACACGT AAGGTCTTAG 3360  
 TGCTTAACAG TTTAAAGGAA AGTCTTGTG GAGGCAGAAC TAAGTTTACA GGGAAGGTA 3420  
 CACACATTCT CTCTCTCT CTCTCTCTCT CTATCTAGTT CCCAGCTTG GAGAGCCTTT 3480  
 CCCCTTGCTT CTCTCTGAGG CCATATAAGC TTATAAGAAA AGTCCCAAAC CAAGAATAGG 3540  
 TCCTTGGCCA CAAGCAGGGT CTGATCCCC ATCAGAGCTA TCTGAGCCTG CTTGTCTGGG 3600  
 CACCTGCTGC AACCATGCG CTACCTGCC AGGGGCACTC AGCAAACAGA ACCACAGGGC 3660  
 CCAGGAGGCA TTCCACACAG GCCTGCCCC AGGACAACAC AACAAAGGACA GTCACACAA 3720  
 GGACAACAAG GACACAACAC AACACAACAC AAGGACAGTC ACAACAAGCC TAGAGCCAGA 3780  
 AAGCAGATGG AAATGCTAAT GAGGTCAAAC GTAGGCTTCA TGGTGGGTGG AGTGGGGGTG 3840  
 GCTGGGCTCC CCCAGGACAG AGGGGACCCT GAGGTTGGCA AGGCTCTCAC CACTCAGCCT 3900  
 TATGTCCTCT TATCTCCTAT CTTCCTCTT GAGAAAATAC ACGCTTCTG CATGTATTAG 3960  
 AAACGCACGA GTCTCCACAA GTCTACAATG AAAGTTGAA ATTAACTGC AAGGAATTAG 4020  
 AAGCATATTT GCAATCATG CAGCTTCTT TTTCTCTGC TCATAAAAGG AGGAACACTT 4080  
 TAGATAGAGG GCAAAATAT CTGAAACCT AATTCTTTC TTTTITGAT AAGGAAATCT 4140  
 TTTCCATCTC CATCTAACA TGCAACACCT GTGAAGAGAA TTGTTCTAT AGTAACTGGT 4200  
 CTGTGATCTT TTGTGGCCAA GAGAATAGCA GGCAAGAAAT AGGGCCTTGA CAGAAITTC 4260  
 ACCAAGCTCT GAGAAGCATG TTGTTCGAA TGCTGATTC CTCTTTGTC TCAATGTGTA 4320  
 TGCTCTGTC CCATCTCTCA CTCTCTCTCA AGCTCACACC AATTGGTTG GCACAGGCAC 4380  
 AGAGCTGGT CCTAGTTAAG TGGCATTAT GTTAAAAAAA AATAGTTTCA AATCTCAGCC 4440  
 TTTTCTTGT GTCATCAAAA CAGCTTAAGA AGGGGACTAC TGCCAATGTC CTCTAGTCTG 4500  
 ACCTCCACCC AGGGAGGACC CATGGCAGGT CTTTCAACT TTCTGATTC TGAGAACAAC 4560  
 CTTGTGAAG TTTTCCCACT TCTAAAGTG TTTCTGATC CTGTCTCTC CTTTGGACCT 4620  
 CACAACAAAT CCTGTGAAGT AACTGAGACA TCTGTGTGTA GATACATTTT TGTGATGAGT 4680  
 AAACGTAGGC TTCG

Seq ID NO: 36 Protein sequence:

Protein Accession #: NP\_071414.1

1 11 21 31 41 51  
 MLPGRLCWVP LLLALGVGSG SGGGGDSRQR RLLAAKVNKH KPWIETSYHG VITENNDTVI 60  
 LDPLVALDK DAPVPFAGEI CAFKIHQEL PFEAVVLNKT SGEGLRLAKS PIDCELOKEY 120  
 TFIQAYDCG AGPHETAWK SHKAVVHIQV KDVNEFAPTF KEPAYKAVVT EGKIYDSILQ 180  
 VEADEDCEP QYSQICNYEI VTIDVPFAID RGNIRNTEK LSYDKQHQYE ILVTAYDCGQ 240  
 KPAAQDTLVQ VDVKPVCKPG WQDWTKRIEY QPGSGSMLP FSHLETCDG AVSSLQIVTE 300  
 LQTNVIGKGC DREYSEKSL QKLCAGSSGI IDLLPSPSAA TNWTAGLLVD SSEMFKFDG 360  
 RQGAIPDGI VPKNLIDQFT ITMWMKHGPS PGVRAEKETI LCNSDKTEMN RHHYALVYHN 420  
 CRLVFLRKD FDQADTFRPA EFHWKLDQIC DKEWHYVYIN VEFPVITLYM DGATYEPYLV 480  
 TNDWPIHPSH IAMQLTVGAC WQGGEVTKPQ FAQFFHGSLA SLTIRPGKME SQKVISCLQA 540  
 CKEGLDINSL ESLGQGIKYH FNPQSILVM EGDDIGNINR ALQKVSYINS RQFPTAGVRR 600  
 LKVSSEKVCF GEDVCISIE VDAYVMVLQA IEPRTLRTG DHFWRPAAQF ESARGVTLFP 660  
 DIKIVSTFAK TEAPGDVKT DPKEVLEEM LHNLDPCDIL VIGGDLDRQ ECLELNHSEL 720  
 HQRHLDATNS TAGYSIYGVG SMSRYEQVLH HIRYRNWRPA SEARFRK CSELNGRYTS 780  
 NEFNLEVSIL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSSVVP SIATVVIHS 840  
 VCMLVFVAM GVYRVRIHQ HFIQETAAK ESEMDWDDSA LTTVNPMEK HEGPGHGEDE 900  
 TEGHEEEAE EEMSSSSGSD DSEEEEEEG MGRGRHGQNG ARQAQLEWDD STLFPY

Seq ID NO: 37 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 143-874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60  
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCTCGGT CTCTCCGCC TCCAGCTCCG 120  
 CGCTGCCCGG CAGCGGGGAG CCATGCGACC CCAGGGCCCC GCGCGCTCC CCGAGCGGCT 180  
 CCGCGGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240  
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGTGGACC TGTATAATGG 300  
 AATGTGCTTA CAAGGCGGAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360  
 CATCCGCGGT ACACCTGGGA TCCAGGTGCG GGATGGATTC AAAGGAGAAA AGGGGGAATG 420  
 TCTGAGGGAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480  
 ATTGAATTAT GGCATAGATT TTGGGAAAA TCGCGAGTGT ACATTACAA AGATGCGTTC 540  
 AAATAGTGCT CTAAAGATT TTGTCAGTGG CTCACCTCGG CTAAAAATGA GAAATGCATG 600  
 CTGTACGCGT TGGTATTTC CATCAATGG AGCTGAATGT TCAGGACCTC TCCCATTGA 660

AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720  
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGTCT GGATTAGTGG ATGTTGCTAT 780  
 CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840  
 TICTCGCATC ATTATTGAAG AACTACCCAAA ATAAATGCTT TAAATTTTCAT TIGCTACCTC 900  
 5 TTTTATTATT ATGCCTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960  
 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020  
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTITTAGT 1080  
 TGGTTAGAAT ACTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140  
 10 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200  
 TGTACAATT GTAAATGTTA AGAATTTTT TTATATCTGT TAAATAAAAA TTAATTTCCAA 1260  
 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 38 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51  
 MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGPITPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 20 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIYLDQ 180  
 GSPENNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRJIEE 240  
 LPK

Seq ID NO: 39 DNA sequence:

Nucleic Acid Accession #: NM\_000949

Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGAGGCTGAA ATCCCCAGAC GCCGGTTTC TGGGCTGGGC TTCTGCTTA CTCACTCCTT 60  
 CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120  
 ATGTCCTCGT GCAGGAAGTA CTATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180  
 TAAAGAACTC TCCTATTTCAT GGAGGCGAAC ACTGAGGATG CTTCCACAT GAACCTGAA 240  
 35 GTGAACCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300  
 CATCTGCAAC CGTTTCACT CTGCTACTTT TTCTCAACAC CTGCCCTCTG AATGGACAGT 360  
 TACCTCTGG AAAACCTGAG ATCTTTAAAT GTCGTCTCC CAATAAGGAA ACATTCACT 420  
 GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCCTACCAA TTATTCACTG ACTTACCACA 480  
 GGGGAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGTGGC CCCAACTCCT 540  
 40 GCCACITTTG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600  
 CTAACCATGAT GGAAGCAGT TCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660  
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAAACA GCCAGAAGAC AGAAAACCTT 720  
 ACCTGTGGAT TAAATGGTCT CCACCTACCC TGAATTGACTT AAAAAGTGGT TGGTTACGCG 780  
 TCCTGTATGA AATTGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840  
 45 GGCAGCAAA AGAGTTTAA ATTTCTAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900  
 TTCGTGCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960  
 TACCTAGTGA CTTACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTTCTG 1020  
 CTGTCATCTG TTTGATTAT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080  
 GCATCTTTCC GCCAGTTCTT GGGCCAAAAA TAAAAGGATT TGATGCTCAT CTGTTGGAGA 1140  
 AGGGCAAGTC TGAAGAACTA CTGAGTGCTT TGGGATGCCA AGACTTTCTT CCCACTTCTG 1200  
 50 TGTCACTCCA TCAAAAGAA CACCCAAAGT AAGGTATGAA ACCCACATAC CTGGATCCTG 1320  
 AACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCTT TTGTCTGAA AAGTGTGAGG 1380  
 AACCACAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAG CCAGAGAATC 1440  
 CTGAAACAAC CCACACCTGG GACCCCCAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500  
 55 TTCTGCTGG TGGATCCAAA TGTCAACAT GGCCTTACC ACAGCCAGC CAGCACAACC 1560  
 CCAGATCCTT TTACCACAA ATTACTGATG TGTGTGAGCT GGCCTGGGC CCTGCAGGTG 1620  
 CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680  
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTTCTGAGA 1740  
 60 CTGACCAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAA CCCCTTTGGC TCCGCTAAAC 1800  
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAAGATGG TGCAATTCA TTGCTACCAA 1860  
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920  
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCCATG 1980  
 CTAAAAACGT GGCTTGCTT GAAGAATCAG CCAAAGAGGC CCACCATCA CTGGAACAGA 2040  
 65 ATCAAGCTGA GAAAGCCCTG GCCAACTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100  
 TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTACACA CTCCTTTTAC TGATAGCTTG 2160  
 ACTAATGGAA TGATTGGTA AAATGTGATT TTCTTCAGG TAACACTACA GAGTACGTGA 2220  
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA 2280  
 70 TTTTAAACA CTGCTCTCT TCTCCAGCAG CTGATTCCAG ACAAATTCAT TATGTTTCT 2340  
 AACTGTGATT TGTAGATTTA CTTTGTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400  
 AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAGG 2460  
 GCCTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATGT TTACCATAGA 2520  
 AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC 2580  
 75 AACTGCATAA CCTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640  
 AAAGAAAGAA TGCATTCCAG AACAAATGT TTACATAAGT TCCTATACCT TACTGACACA 2700  
 TTGCTGATAT GCAAGTAAGA AAT

Seq ID NO: 40 Protein sequence:



Protein Accession #: NP\_000940.1

1 11 21 31 41 51  
 5 MKENVASATV FTLLLLNTLC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGLPNTY 60  
 SLTYHREGET LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNATNQMG SSFSDELYVD 120  
 VTYIVQDPP LELAVEVKQF EDRKPYLWIK WSPPTLIDLK TGWFILLYEI RLKPEKAAEW 180  
 EIHFAQQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP AIFIQIPSDF TMNDTTVWIS 240  
 10 VAVLSAVICL IYWAVALKG YSMVTCIFPP VPGPKIKGFD AHLLEKGSB ELLSALGCQD 300  
 FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDPDITDSG RGSCDSPSL 360  
 SEKCEFPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420  
 PSQHNPRSSY HNTDVCLELA VGPAGAPATL LNEAGKDALK SSQTKSREE GKATQQREVE 480  
 SFHSETDQDT PWLLPQEKTP FGSAPKLDYV EHKVNKDGA LSLPKQREN SGKPKKPGTP 540  
 15 ENNKBYAKVS GVMDDNLLYL VPDPAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600  
 KCRLQLGGLD YLPACFTHS FH

Seq ID NO: 41 DNA sequence

Nucleic Acid Accession #: none found, Eos cloned sequence

Coding sequence: 1-1572 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 20 ATGACCCAAA ATAAATTAAA GCTTTGTTCC AAAGCCAATG TGTATACTGA AGTGCCTGAT 60  
 GGAGGATGGG GCTGGGCGGT AGCTGTTTCA TTTTCTTCG TGAAGTCTT CACCTACGGC 120  
 25 ATCATCAAGA CATTGGTGT CTCTTTAAT GACITAATGG ACAGTTTAA TGAATCCAAT 180  
 AGCAGGATCT CATGGATAAT CTCATCTGT GTGTTTGTCT TAACATTTC AGTCCCTC 240  
 GCCACAGTCC TGAACAATCG TTTCGGACAC CGTCTGGTAG TGATGTTGGG GGGGCTACTT 300  
 GTCAGCACCG GGTGTTGGG CGCCTCCTTC TCACAAGAGG TTTCTCATAT GTACGTCGCC 360  
 30 ATCGGCATCA TCTCTGGTCT GGGATACTGC TTAGTTTTC TCCCACTGT AACCATCCTA 420  
 TCACAATATT TTGGCAAAAG ACGTTCATA GTCACTGCAG TTGCTTCCAC AGGAGAATGT 480  
 TTGCTGTGT TTGCTTTCG ACCAGCAATC ATGGCTCTGA AGGAGCGCAT TGGCTGGAGA 540  
 TACAGCCTCC TCTCTGGTGG CTTACTACAG TTAACAATG TCATCTTCG AGCACTGCTC 600  
 AGACCCATCT TTATCAGAGG ACCAGCGTCA CCGAAAATAG TCATCCAGGA AAATCGGAAA 660  
 35 GAAGCGCAGT ATATGCTTGA AAATGAGAAA ACACGAACCT CAATAGACTC CATTGACTCA 720  
 GGAGTAGAAC TAACACTCTC ACCTAAAAAT GTGCCTACTC ACCTAACCT GGAAGTGGAG 780  
 CCGAAGGCGG ACATGCAGCA GCTCCTGGTG AAGACCAGCC CCAGGCCAAG CGAAAAGAAA 840  
 GCCCGCTAT TAGACTTCTC CATTITGAAA GAGAAAAGTT TTAATTGTTA TGCATTATT 900  
 40 GGTCTCTTTG CAACACTGGG ATTCCTTGA CTTCTCTGT ACATCATTC TCTGGGCATT 960  
 AGTCTGGGCA TTGACCAGGA CCGCGCTGCT TTTTATTAT CTACGATGGC CATTGCAGAA 1020  
 GTTTTCGAAA GGATCGGAGC TGGTTTGTG CTCAACAGGG AGCCCATTCG TAAGATTTC 1080  
 45 ATTGAGTCA TCTGCGTCA TTTATTGACT GTGCTCTGT TTGCTTTAC TTTTGTACT 1140  
 GAATCTGGG GTCTAATGTC ATGCAGCATA TTTTGGGT TATGTTGG AACAATAGGA 1200  
 GGGACTCACA TTCCATGCT TGCTGAGGAT GATGTCGTGG GCATTGAGAA GATGCTCTCT 1260  
 GCAGCTGGGG TCTACATCTT CATTGAGAGC ATAGCAGGAC TGGCTGGACC GCCCTTGA 1320  
 50 GGTCTGTGG TGGACCAAAG TAAGATCTAC AGCAGGGCCT TCTACTCTG CGCAGCTGGC 1380  
 ATGGCCCTGG CTGCTGTGTG CCTCGCCCTG GTGAGACCGT GTAAGATGGG ACTGTGCCAG 1440  
 CATCATCACT CAGGTGAAAC AAAGGTAGT AGCCATCGT GGAAGACTT ACAGGCATCA 1500  
 CCTGAAGACT TTCTGAAAT GGATCTTGA AAAATGAGC ACAGAGTCA CGTGCAAAATG 1560  
 GAGCCGGTATGA

Seq ID NO: 42 Protein sequence:

Protein Accession #: none found, Eos cloned sequence

1 11 21 31 41 51  
 55 MTQNKILCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IKTFGVFFN DLMDSFNESN 60  
 SRISWISIC VFVLTFSAPL ATVLNRFH RLVMGLGGL VSTGMVAASF SQEVSHMYVA 120  
 IGHSGLGYC FSFLPTVIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR 180  
 60 YSLLFVGLLQ LNIIVPGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240  
 GVLELTSPKN VPHTNLELE PKADMQQVLV KTSRPSSEK APLDLSILK EKSIFYALF 300  
 GLFATLGFFA PSYIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360  
 65 IELICVILIT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GTHIPLAED DVVGIEKMSS 420  
 AAGVYIFQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480  
 HHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 43 DNA sequence

Nucleic Acid Accession #: FGENESH predicted ORF

Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 70 ATGCTGTCTG GCTTCTGAT GAGTCCCAGT ACCCAGCACA GAGCAGAGTA CACTCCCGGA 60  
 GGAAAGAAAC TTCCGTGGGA GGCITCCAAT GGTGCGCACA CCTCCGAGG GCGAGGCAGC 120  
 75 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGCG CGCCAGCTGG GCAGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCC 300  
 CGCCTGCGTC CTGGACGTT CCGGGGGAGG GTCCGGTTC CAGTGAAACC TCCAGAGGCT 360

TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCCTGGAC CTAGGCCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCCGCGG GACAGTCACT GACGAGGGCC GGGGGTCGCC GGGGCCACGA 600  
 5 CTCTCTGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCGCTCG TCGTCTCTCT CATCTGGAA CGCCGCTTCG CTCTGCAGC 720  
 TGCTGCTGGC TCGCTGCTG GCGCGGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 10 GCGGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900  
 GCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGCGCTGG CGAGCCTGGC 960  
 CCGGCGGACA AAGACGGGCG CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGTACCCAA 1020  
 GGAGACGGCG AGGGTGGGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCTGAAGGC 1080  
 TCCCGAAGG GAAGGCAGCT CCTCAGGGCT TCCCGGGGCG TGCTGCCCGG TGCCAGACGC 1140  
 CGCGATTCC CATCTCTCC ACGCGCGGCG CCTCTCCCG TGCAGCGGCC CGCTTGCC 1200  
 15 ATCTACGTGC CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CCTTTATCAT CTGGGGTCC 1260  
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 CCGGGGTCGT CCTCAGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAACCTC 1440  
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 20 AACAAGTGT ATGTCACCT GCGACGAAT TTCTCTGTG TGAAGTGA CAGAGGCCAC 1560  
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 AGGAGATTG AGTCCCGCTT CCTCAGACC AACAGTGAAC AGAAGATGA CCCAGCGGTG 1740  
 25 ACTGTATAAC CGAGAGTCAC TGGTGGGTC CTCTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGGTATTGA TGGCAGGAT CCTTTGGATG 1860  
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 TTGCTGATGG GTGTATAACA AATGCTTGA TCCGAAGTGC CCTGAGATA TGGTTGACGA 2040  
 30 AAGAATTGA TAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100  
 TTGTTGTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTT 2160  
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Seq ID NO: 44 Protein sequence:

Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
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 60 MLGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 65 GEAEKGNRGE PPAWIRAQQ PRPPAGQAP GTAAGGAQDP RLRPGRGR VRLPVKPPEA 120  
 SGRQPRGSPD CIPRFSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAABGSG 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALAPRVVP CGALAARPS HPGTPLRSCS 240  
 CCWLRCWRRO RGPSEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSAE 300  
 70 ARLDQGGCDN DRQQAGGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPV RAWQRCSPG 360  
 SPKGRQLLRA PFGLLPRARR RGFSSPRGG PSPLQRPALP IYVFFLVGS VFVAFILGS 420  
 LVAACCRCL RPKQDQQRK APGGRNLMET IPMPSASTS RGSRRQSSST AASSSSANS 480  
 GARAPPTRSQ TNCCLPBTM NNIVYNMPTN FSVLNCQQAT QIVPHQGYL HPPYVGYTVQ 540  
 HDSVPMATAVP PFMDGLQPGY RQIQSPFPH NSEQKMPYAV TV

Seq ID NO: 45 DNA sequence

Nucleic Acid Accession #: NM\_092285

Coding sequence: 55-3738 (underlined sequences correspond to start and stop codons)

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 5 GGCGAGCCT CGCGGCGCG GGTAGCGGCG GCGGCGACGC TGACACCTCC CACCATGGAC 60  
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 GATGGCACGT TTAATTCTAG TTAATCTCTC TTCAGTGAGC CCTACAAGAC TAACAAGGGG 240  
 GATGAATCTT CCAACCGGAT CCAGAACACT TTAGGCAATT ATGATGAAAT GAAAGACTTT 300  
 TTAATCTGATA GAACCAATCA GAGTCATCTC GTTGGAGTTC CCAAACCTGG GGTTCCTCAG 360  
 10 ACTCCTGTGA ACAAGATCGA TGAACATTTT GTTGCAGATT CAAGAGCCCA GAACCAAGCCC 420  
 TCGTCTATCT GTAGCACTAC AACTCCACA CCAGCAGCTG TCCCGTGCA GCAGAGTAAA 480  
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 ACACAACAGG GCTCTCTCAG GACCTTGCTT GGAGATGGTG TTGGCAGACA GCAGCCTCGG 600  
 GCCAAACAAG TGTGCAATGT GGAGGTGGGC CTTCAGACCC AGGAGAGGCC ACCTGCCATG 660  
 GCGGCCAAGC ACAGCAGCAG CGGACACTGT GTTCAGAACT TTCCTCCATC CTTAGCTTCA 720  
 15 AAACCCAGCG TGCTCAGCA GAAACCGACC GCGTATGTGA GGCCAATGGA CCGCCAAGAT 780  
 CAGGCCCCCTG ATGAGTCTCC TAAGCTGAAG TCGTCTTCGG AAACCAAGCGT GCACTGCACA 840  
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 20 AAAGTGAAC CAACCAAT TCCATTCCA AATAAGGACT CTCAGCTTGT ATCCTCTGGA 1080  
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 ACATCAATGC TGAAGATGA CCTTAAGCTA AGCAGTGATG AAGAGGAGAA TGAACAGCAG 1200  
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 GCATTATGTT ACCGATGCTT GGCCTCTCTG TACTGGCGGA GTTTTCGACT CAAAAGGGAC 3300  
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 60 CAAGCCCCAT CTCGTGGGG GGCCAGTGG AAGAGCACTG GAACCCCATC CCCCATTCT 3420  
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 GTCAGCATCA CCAACAGCAT CCGCACAGC TACGACTACT GGGAGATGGC CGACAACCTG 3600  
 GCCAAGGAAA ACCGAGAAIT CTCAACGAC CTGGATCTGC TCATGGGGCC GGTACCCCTG 3660  
 65 CACAGCACA TGGAGCACTT GGTCCAGTAC TCCCAACAGG GCTGCACTG GCTCGGAAAC 3720  
 AGCGCCACC TGTCATAGGG ACCTACCCCT GGGGCCAGAG TGGGCTCTGG TCTCCACAGA 3780  
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 CCGTGAACAT TTCTCA

Seq ID NO: 46 Protein sequence:  
 Protein Accession #: NP\_002276

1 11 21 31 41 51  
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 75 MDSFDLALLQ EWDLESICVY EPDRNALRRK ERERRNQETQ QDDGTFNSSY SLFSEPYKTN 60  
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 PRAKQVCNVE VGLQTQERFP AMAAKHSSSG HCVQNFPSL ASKPSLVQK PTAYVRPMDG 240

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 CVEEIREMT WLPPLSAQI PGKVEPTKFP FPNKDSQLVS SGHNNPKKGD AEPESPDNGT 360  
 SNTSMLEDDL KLSDBEENE QQAARTALR ALSDSAVVQQ PNCRTSVPS KSSSSSSSG 420  
 TSSSSSDSES SSGSDSETES SSSSESGSKP PHFSSPEAEP ASSNKWQLDK WLNKYNPHKP 480  
 PILIQNESHG SESNQYYPV KEDVQDCGKV PDVCQPSLRE KEIKSTCKEE QRPRTANKAP 540  
 GSKGVKQKSP PAAVAVAVSA AAPPAVPCA PAENAPAPAR RSAGKKPTRR TERTSAGDGA 600  
 NCHRPPEEPAA ADALGTSVVV PPEPTKTRPC GNNRASHRKE LRSSVTCEKR RTRGLSRVP 660  
 KSKFETES SSSSSSDSD LESEQEYPL SKAQTVASA SSGNDQRLKE AAANGSGSPR 720  
 APVGSINART TSDIAKELEB QFYTLVPFGR NELLSPKDS DEIRSLWVKI DLTLRSRIPE 780  
 HLPQEPGVLS APATKDSESA PPSHTSDIPA EKALPKSKRK RKCDNEDDYR EIKKSQGEKD 840  
 SSSRLATSTS NTLNANHCNM NINSVAIPN KNEKMLRSP SPLSDASKHK YTSBDLTSS 900  
 RPNNGSLFIS ASSSKPKAD SQLPHGGDL TKAHNHNSN IPLHKSRLPQT KPWSPGSNH 960  
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 GPMESKSPYY LMYSETVELI RYAMRLKTHS GPNATPEDKQ LAALCYRCLA LLYWRMFLK 1080  
 RDHAVKYSKA LIDYFNSSK AAQAPSPWGA SGKSTGTPSP ISPNFPFGSS VGSQGLSNA 1140  
 SALSPSTVS IPQRHQMMA NHVSITNSIL HSYDYWEMAD NLAKENREFF NDLDLLMGPV 1200  
 TLHSSMEHLV QYSQGLHLWL RNSAHL

Seq ID NO: 47 DNA sequence

Nucleic Acid Accession #: NM\_033151

Coding sequence: 351-4499 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 25 | | | | |  
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 ACTAAGTGAT TTGGGCTGA GGCCTGAGAA GATGTTTAAA AAGAGGGATC AAGCACAGGC 180  
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 30 GTAGTGCCCC CTCCTCTGGC TGCTCAAGGC GAGATCTAAG CTTCTCTAA CTCCTGCTGT  
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 GCGATGACAT GGTTCAGGA CTATTATTA AAACCTATAC TCTCCAAGAT GGCCCTGGA 480  
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 35 ATGATGCTGC CTTGAGAACC ATGATTCCT TCGTCCCAA GCGAGGTTT CCGTCCCCC 600  
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 ATGCTCAGA CAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA GTCTCAAGGC 780  
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 45 AGAAGCTCAT CCAATTAAAG TGTGTAATAC ACATCACCTC AGGAGAGGCC ATCAGCTTCT 1140  
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 50 TCATTGAAG CTTAAGAAGG AAGGAAAGGA AACTATTGGA GAATGCGGG CTTGTCCAGA 1500  
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 55 TCCAGACATT ACAAGACCC AGCAAGGCTC TGGTCTTGA GGAGGCCACC TTGTCATGGC 1800  
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 TCTCAAGACG TTAGAACCCC AGAACCATCT AAGACATGGG ATTCAGTGAT CATGTGGTTC 4740  
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 TC

Seq ID NO: 48 Protein sequence:  
 Protein Accession #: NP\_149163.2

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 VNGALELERNGHASSEGMRPRDALGPBEGNSLGPFLHKINLVVSKGMMGLVCGNTGSGKSSLLSAILLE  
 MHLLEGSVGVQGSLAYVPPQAWIVSGNIRENIMGGAYDKARYLQVLHCCSLNRDLELLPFGDMTEIGER  
 GLNLSGGQKQRISLARA VYSDRQIYLLDDPLSAVDHVGKHIFECIKTLRGKTVVLTHTQLQYLEFCG  
 QILLENKICENGTHSELMQKKGYAQLIQMKHEATSDMLQDTAKIAKPKVESQALATSLEESLNGN  
 AVPEHQLTQEEEMEGSLSWRVYHHYIAAGGYMVSCIFFVVLVLTIFSFVWLSYWLQGGSGTNS  
 RESNGTMADLGNADNPQLSFYQLVYGLNALLICVGVCSGIFTKVRKASTALHNKLFNKVFRCPMSF  
 FDTIPIGRLNCFAGDLQLDQLLPFSEQLVLSLMVIAVLLVSVLSPYILLMGAIMVICFTYMMF  
 KKAIGVFKRLNYSRSLFSLHLSLQGLSSIHVYKTEDFISQFKRLTDAQNNYLLFLSSTRWMAALRL  
 EIMTNLVTALVALFVAFGISSTPYSFKVMAVNIVLQLASSFQATARIGLEBAFTAVERILQYMKMCVS  
 EAPLHMEGTSCPQGWPFQHGHIIFQDYHMKYRDNTPTVLHGNIITRIGHEVVGVIGRTGSGKSSLMALFR  
 LVBFMAGRILIDGVDCISIGLEDLRSKLSVTPQDPVLLSGTIRFNLDPFDRHDTQIWDALERTFLTKAI  
 SKFPKLLHTDVVENGNFSVGERQLLCIARAVALRNSKIILIDEATASIDMETDILQRTIREAFQGCFTVL  
 VIAHRVTVLNCDHILVMGNGKVVEEDRPEVLRRKPGSLFAALMATATSSLR

Seq ID NO: 49 DNA sequence  
 Nucleic Acid Accession #: NM\_033419  
 Coding sequence: 18-980 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGAGCCAGGG AGAAAGGATG GCCGGCCTGG CGGCGCGGTT GGTCTGCTA GCTGGGGCAG 60  
 CGGCGCTGGC GAGCGGCTCC CAGGGCGACC GTGAGCCGGT GTACCGCGAC TGCGTACTGC 120  
 AGTGGGAAGA GCAGAACTGC TCTGGGGGCG CTCTGAATCA CTTCGCTCC CGCCAGCCAA 180  
 TCTACATGAG TCTAGCAGGC TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240  
 TCACCGTTGG GCTCTACCTC CAGGAAGGTC ACAAAGTGCC TCAGTTCCAT GGCAAGTGGC 300  
 CCTCTCCTCC GTTCTGTTC TTCAAGAGC CGGCATCGGC CGTGGCCTCG TTTCTCAATG 360  
 GCCTGGCCAG CTTGGTGATG CTCTGCGGCT ACCGCACCTT CGTGCCAGCC TCCTCCCCCA 420  
 TGTACCACAC CTGTGTGGCC TTGCGCTGGG TGTCCCTCAA TGCATGGTTC TGGTCCACAG 480  
 TTTTCCACAC CAGGGACACT GACCTCACAG AGAAAATGGA CTACTCTGT GCCTCCACTG 540  
 TCATCCTACA CTCAATCTAC CTGTGCTGCG TCAGGACCGT GGGGCTGCAG CACCCAGCTG 600  
 TGGTCAGTGC CTTCGGGCT CTCTGCTGCT TCATGCTGAC CGTGACGCTC TCCTACCTGA 660  
 GCCTCATCCG CTGCTACTAT GGCTACAACC TGGTGGCCAA CGTGGCTATT GGCCTGGTCA 720  
 ACGTGGTGTG GTGGCTGGCC TGGTGCCTGT GGAACACGCG GCGGCTGCTC CACGTGCGCA 780  
 AGTGGCTGGT GGTGGTCTTG CTGCTGCAGG GGCCTGCTCT GCTCGAGCTG CTTGACTTCC 840  
 CACCGCTCTT CTGGGTCTTG GATGCCCATG CCATCTGGCA CATCAGCACC ATCCTGTGCC 900  
 ACGTCTCTTT TTTACGCTTT CTGGAAGATG ACAGCCTGTA CCGTCTGAAG GAATCAGAGG 960

ACAAATTCAA GCTGGACTGA AGACCTTGGG GCGAGTCTGC CCCAGTGGGG ATCCTGCCCC 1020  
 CGCCCTGCTG GCCTCCCTTC TCCCTCAAC CCTTGAGATG ATTTTCTCTT TTCAACTTCT 1080  
 TGAACCTTGA CATGAAGGAT GTGGGCCAG AATCATGTGG CCAGGCCACC COCTGTTGGC 1140  
 CCTCACCAGC CTTGAGTCT GTTCTAGGGA AGGCTCCCA GCATCTGGGA CTCGAGAGTG 1200  
 GGCAGCCCT CTACCTCTG GAGCTGAAC TGGGTGGAAC TGAGTGTGCT CTTAGCTCTA 1260  
 CCGGAGGAC AGCTGCCTGT TTCTCCCA TCAGCCTCT CCCCACATCC CCAGCTGCCT 1320  
 GGCTGGGTCC TGAAGCCCTC TGTCTACCTG GGAGACCAGG GACCACAGGC CTTAGGGATA 1380  
 CAGGGGGTCC CCTTCTGTTA CCACCCCCCA CCTCTCTCCA GGACACCACT AGGTGGTGCT 1440  
 GGATGCTTGT TCTTGGCCA GCCAAGGTTT ACGGCGATTC TCCCATGGG ATCTTGAGGG 1500  
 ACCAAGCTGC TGGGATTGGG AAGGAGTTT ACCCTGACCA TTGCCCTAGC CAGGTTCCCA 1560  
 GGAGGCTCA CCATCTCTCC TTTGAGGGCC AGGGCTCCAG CAAGCCAGG GCAAGGATCC 1620  
 TGTGCTGCTG TCTGTTGAG AGCCTGCCAC CGTGTGTCGG GAGTGTGGC CAGGCTGAGT 1680  
 GCATAGGTGA CAGGGCCGTG AGCATGGGC TGGGTGTGTG TGAGTCAAG CTTAGGTGCG 1740  
 CAGTGTGGAG ACGGGTGTG TCGGGGAAGA GGTGTGGCTT CAAAGTGTGT GTGTGCAGGG 1800  
 GGTGGGTGTG TTAGCTGGG TTAGGGGAAC GTGTGTGCGC GTGCTGGTG GCATGTGAGA 1860  
 TGAGTGACTG CCGGTGAATG TGTCCACAGT TGAGAGGTG GAGCAGGATG AGGGAATCCT 1920  
 GTCACCATCA ATAATCACTT GTGGAGGCC AGCTCTGCC AAGGCCAC CTGGGCGGAC 1980  
 AGCCAGGAGC TCTCATGGC CAGGCTGCC GTGTGCATGT TCCCTGTCTG GTGCCCTTT 2040  
 GCCCGCTCC TGAAACCTC ACAGGCTCC CACACAACAG TGCCCTCCAG AAGCAGCCCC 2100  
 TCGGAGGCAG AGGAAGGAAA ATGGGATGG CTGGGGCTCT CTCCATCCTC CTTTCTCTCT 2160  
 TGCCTGCGA TGGTGGCTT TCCCTCCAA AACCTCCATT CCCCTGTGC CAGCCCCCTT 2220  
 GCCATAGCCT GATTTTGGG AGGAGGAAAG GCGGATTGA GGGAGAAGGG GAGAAAGCTT 2280  
 ATGGCTGGGT CTGGTTCTT CCCTTCCAG AGGGTCTTAC TGTCCAGGG TGGCCCCAGG 2340  
 GCAGGCAGGG GCCACACTAT GCCTGCGCCC TGGTAAAGGT GACCCCTGCC ATTTACCAGC 2400  
 AGCCCTGGCA TGTCTCTGCC CCACAGGAAT AGAATGGAGG GAGCTCCAGA AACTTTCCAT 2460  
 CCAAAGGCA GTCTCGGTG TGAAGCAGA CTGGATTTT GCTCTGCCCC TGACCCCTTG 2520  
 TCCCTCTTG AGGGAGGGGA GCTATGCTAG GACTCCAACC TCAGGGAATC GGGTGGCCTG 2580  
 CGTAGCTTC TTTGATACT GAAAACTTT AAGGTGGAG GGTGGCAAGG GATGTGCTTA 2640  
 ATAAATCAAT TCCAAGCCTC AAAAAAAAA AAAAAAAAA AA

Seq ID NO: 50 Protein sequence:

Protein Accession #: NP\_219487.1

1 11 21 31 41 51  
 | | | | |  
 MKDVGPESCG QPTPCWPSA LESVLGKASQ HLGLESQPL YLLELNWGGT ECALSSSTGR 60  
 AACFLPISLL PTSPAAWLPG EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTRWCWMLV 120  
 LWPAKVHGDG PHGLLRDQAA GIGKEFHPDH CPSQVPRRPH HTPFQGGSS KPRARILCCC 180  
 LVESLPPCVG SVGQAECIGD RAVSMGLGVC ELRPRCAVWR RVLSGKRQCF KVCVCRGWVC

Seq ID NO: 51 DNA sequence

Nucleic Acid Accession #: XM\_059098.1

Coding sequence: 178-518 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GATGTACACT CTGAAGTGAG CACATTCTG TTGGCAGGAC ATGACACCTT GGCAGCAAGC 60  
 ATCTCTGGA TCTTTACTG CTTGGCTCTG AACCTGAGC ATCAAGAGAG ATGCCGGGAG 120  
 GAGGTACAGG GCATCTGGG GGATGGGTCT TCTATCACTT GGGACCAAGT GGGTGAGATG 180  
 TCGTACACCA CAATGTGAT CAAGGAGAGC TGCCGATTGA TTCTGCACT CCCGTCCATT 240  
 TCCAGAGATC TCAGCAAGCC ACTTACCTTC CCAGATGGAT GCATATGCC TGCAGGGATC 300  
 ACCGTGGTTC TTAGTATTG GGGTCTTCAC CACAACCCCTG CTGTCTGGAA AAACCCAAAG 360  
 GTCTTTGACC CCTTGAGGT CTCTCAGGAG AATTCTGATC AGAGACACCC CTATGCCTAC 420  
 TTACCATCT CAGCTGGATC AAGGAAGTGC ATTGGGCAGG AGTTGCCAT GATTGAGTTA 480  
 AAGGTAACCA TTGCCCTGAT TCTGCTCCAC TTCAGAGTGA CTCAGACCC CACCAGGCCT 540  
 CTACTTCTC CCAACCATTT TATCTCAAG CCCAAGAATG GGATGTATT GCACCTGAAG 600  
 AAACCTCTG AATGTTAGAT CTCAGGGTAC AATGATTAAA CGTACTTGT TTTTCAAGT 660  
 TAAATTTACA GCTAATGATC CAAGCAGATA GAAAGGGATC AATGTATGTT GGGAGGATTG 720  
 GAGGTGGTG GGATAGGGGT CTCTGTGAAG AGATCCAAAA TCATTCTAG GTACACAGTG 780  
 TGTGAGCTAG ATCTGTTCT ATATAACTTT GGGAGATTIT CAGATCTTT CTGTAAACT 840  
 TTTACTACTA TTAATGCTGT ATACACCAAT AGACTTTCAT ATATTTCTG TTGTTTTAA 900  
 AATAGTTTC AGAATTATGC AAGTAATAAG TGCATGTATG CTCACGTCA AAAATTCCCA 960  
 ACACTAGAAA ATCATGTAGA ATAAAAATTT TAAATCTCAC TTCACTTAGC CGACATTCCA 1020  
 TGCCTGACC AATCTACTG CTTTCTCTAA AAACAGAATA ATTTGGTGTG CATTCTTCA 1080  
 GACTTTTCC TATACATTTT ATATGTAGAA ATGTAGCAAT GTATTTGTAT AGATGTGATC 1140  
 ATCTCTATAT TGTATTGAT TTTTTCAC TAATAAAAA TCACCTTATT CCTT

Seq ID NO: 52 Protein sequence:

Protein Accession #: XP\_059098.1

1 11 21 31 41 51  
 | | | | |  
 MSYTTMCIKE TCRIPAVPS ISRDLSPKPLT FPDGCTLPAG ITVVLISWGL HINPAVWKNP 60  
 KVEDPLRFESQ ENSDQRHPYA YLPFSAGSRN CIGQEFAMIE LKVITIALILL HFRVTPDPTR 120  
 PLTFNHFIL KPNKMGMYLHL KKLSEC

Seq ID NO: 53 DNA sequence

Nucleic Acid Accession #:

NM\_030916

Coding sequence: 1-1533 (underlined sequences correspond to start and stop codons)

5     1     11     21     31     41     51  
 |     |     |     |     |     |  
 ATGCCCTGT CCCTGGGAGC CGAGATGTGG GGGCCTGAGG CCTGGCTGCT GCTGCTGCTA 60  
 CTGCTGGCAT CATTACAGG CCGGTGCCCC GCGGGTGAGC TGGAGACCTC AGACGTGGTA 120  
 10     ACTGTGGTGC TGGGCCAGGA CGCAAACTG CCTGCTTCT ACCGAGGGGA CTCCGGCGAG 180  
 CAAGTGGGGC AAGTGGCATG GGCTCGGGTG GACGCGGGCG AAGGCGCCCA GGAAGTAGCG 240  
 CTACTGCACT CCAATACGG GCTTCATGTG AGCCCGGCTT ACGAGGGCCG CGTGGAGCAG 300  
 CCGCCGCCCG CACGCAACCC CTTGGACGGC TCAGTGCTCC TGGCAACGC AGTGCAGGCG 360  
 GATGAGGGCG AGTACGAGTG CCGGGTCAGC ACCTTCCCCG CCGGCAGCTT CCAGGCGCGG 420  
 CTGCGGCTCC GAGTGCTGGT GCCTCCCCTG CCCTCACTGA ATCCTGGTCC AGCACTAGAA 480  
 15     GAGGGCCAGG GCCTGACCTT GGCAGCCTCC TGCACAGCTG AGGGCAGCCC AGCCCCCAGC 540  
 GTGACCTGGG ACACGGAGGT CAAAGGCACA ACGTCCAGCC GTTCTTCAA GCACTCCCGC 600  
 TCTGCTGCCG TCACCTCAGA GTTCCACTTG GTGCTAGCC GCAGCATGAA TGGGCAGCCA 660  
 CTGACTTGTG TGGTGTCCCA TCTGGGCTG CTCCAGGACC AAAGGATCAC CCACATCTC 720  
 CACGTGCTCT TCCTTGTGA GGCCTCTGTG AGGGGCCCTG AAGACCAAAA TCTGTGGCAC 780  
 20     ATTGGCAGAG AAGGAGCTAT GCTCAAGTGC CTGAGTGAAG GGCAGCCCCC TCCTCATAC 840  
 AACTGGACAC GGCTGGATGG GCCTTGCCG AGTGGGGTAC GAGTGGATGG GGACACTTTG 900  
 GGCTTTCCCG CACTGACAC TGAGCACAGC GGCATCTACG TCTGCCATGT CAGCAATGAG 960  
 TTCTCCTCAA GGGATTCTCA GTTCACTGTG GATGTTCTT ACCCCAGGA AGACTCTGGG 1020  
 AAGCAGGTGG ACCTAGTGTG AGCCTCGGTG GTGGTGGTGG GTGTGATCGC CGCACTCTTG 1080  
 25     TCTGCCITTC TGGTGGTGGT GGTGGTGTCT ATGTCCGAT ACCATCGGCG CAAGGCCAG 1140  
 CAGATGACCC AGAAATATGA GGAGGAGCTG ACCGTGACCA GGGAGAACTC CATCCGGAGG 1200  
 CTGCATTCCC ATCACACGGA CCCAGGAGC CAGCCGGAGG AGAGTGTAGG GCTGAGAGCC 1260  
 GAGGGCCACC CTGATAGTCT CAAGGACAAC AGTAGCTGCT CTGTGATGAG TGAAGAGCCC 1320  
 GAGGGCCGCA GTTACTCCAC GCTGACCACG GTGAGGGAGA TAGAAACACA GACTGAACTG 1380  
 30     CTGTCTCCAG GCTCTGGGCG GGCCGAGGAG GAGGAAGATC AGGATGAAGG CATCAAACAG 1440  
 GCCATGAACC ATTTTGTGTA GGAGAATGGG ACCCTACGGG CCAAGCCAC GGGCAATGGC 1500  
 ATCTACATCA ATGGCGGGG ACACCTGGTC TGA

Seq ID NO: 54 Protein sequence:

Protein Accession #:

NP\_112178.1

35     1     11     21     31     41     51  
 |     |     |     |     |     |  
 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE 60  
 40     QVQQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPRNPLDG SVLLRNAVQA 120  
 DEGEYECRVS TYPAGSFQAR LRLRLVPPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS 180  
 VTWDTVEKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHFGL LQDQRITHIL 240  
 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGGPPPSY NWTRLDGPLP SGVRVDGDTL 300  
 45     GFPLITTEHS GIYVCHVSNE FSSRDSQVTY DVLDPQEDSG KQVDLVASV VVVGVAIAL 360  
 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRL LHSHTDPRS QPEESVGLRA 420  
 EGHPSLKDND SSCSVMSEEP EGRSYSTLT T VREIETQTEL LSPGSGRAEB EEDQDEGIKQ 480  
 AMNHVFQENG TLRKPTNG YINRGHLY

Seq ID NO: 55 DNA sequence

Nucleic Acid Accession #:

AF007170.1

Coding sequence: 73-1725 (underlined sequences correspond to start and stop codons)

50     1     11     21     31     41     51  
 |     |     |     |     |     |  
 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60  
 CTGGACCACT GCATGACCGC CCTGGACCTC TTCTCACCA ACCAGTTCTC AGAAGCCTC 120  
 AGCTACCTCA AGCCAGAAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180  
 CTGGAGATAG AGGCCATTGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240  
 60     ATGAAGGAGG CACAGATGCT GTGTCAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300  
 TTCAGCAGCC TGGTGAACCG CCCACGCTG GGCCAAATCA CTGAAGAAGA AATCCACGCT 360  
 GAGGTCTGCT ATGCAGAGTG CTTGCTGCAG CGAGCAGCCC TGACCTTCTC GCAGGACGAG 420  
 AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480  
 GAGCTGGACA GCCTTGTGTA GTCTCACA TACTGCAAGG GTGAGAACA CCCGCACCTT 540  
 65     GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600  
 AGGATCCTGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660  
 CAGCTGGAGG AGGGAGCGTC AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720  
 CTGTGCTACC ACACCTTCTT CACCTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG 780  
 GCCGAGAAGC TCTGAAGCC CTACCTGAAC CGGTACCTA AGGATGCCAT CTCTCTGTTT 840  
 TTTGCAGGGA GGATTGAAGT CATTAAGGC AACATTGATG CAGCCATCCG GCCTTTCGAG 900  
 70     GAGTGTGCTG AGGCCAGCA GCACGTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960  
 ATGTGGTGTG TCACCTCAA GGCACAGTGG AAGATGTCTT ACTTCTACGC CGACCTGCTC 1020  
 AGCAAGGAGA ACTGCTGGTC CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC 1080  
 ATGTTTGGGA AGGAGGACCA CAAGCGTTC GGGGACGACG AAGTGGAAAT ATTTGAGCT 1140  
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200  
 75     CGGAAGTCCC GGCCTACTT CTCTCCAAC CTTATCTCGC TGCCAGTGCC TGCTCTGGAA 1260  
 ATGATGTACA TCTGGAACGG CTACGCCGTG ATTGGGAAGC AGCCGAAACT CAGGATGGG 1320  
 ATACTTGAGA TTACTACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCGAGA GAACGAGTAC 1380

TCAGTGGATG ACGAGTGCTT OGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440  
 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500  
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCTGCTGCT TATGGAGCAA 1560  
 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAACTA CAAGAATTAC 1620  
 TCCATGGAGT CAAGGACACA CTTTCGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680  
 CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740  
 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCTT 1800  
 CCCCCGCCC TGCCTGCTT TTGGGGTCCA CCGGCACTCC AGTGGATGG CACAACATAG 1860  
 TGTATCCGTG CAGAAGCCGA GCTGGCATTT TCACCACTGT AGCCAAGGGC CTTTGCCAAG 1920  
 GGCAGAGCAG GTGGAGCCCT CTGCCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980  
 GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCTT TAGAAATACA TTGATGGGAT 2040  
 CACAGTTGGC TTTAAAAACC AACAACAATC AACCACCTGT AAGTCTTTGT CTTCACCTAT 2100  
 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAATTG CTTTTCAAAT 2160  
 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCCTCAGA GGACCTGAGG AATGCCTGGG 2220  
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTTGGGC ATGAGGATGT ACACAGACAC 2280  
 CCACTACCTT ACTACTCACA CTTCATTICA CTCTTTTGT AAATTTCCAA TTTAAAAATC 2340  
 AAGCAGCTCT TTTAGTAGAG ATAAATCTGT AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400  
 AGTAGAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460  
 AAATTTGGGG GGCAGGAGGA GGTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520  
 CTGAAACCAC TGGGAATAAT TTATGAAACA TAAAAATCTT CTGACTTCA CTCCAAGGTA 2580  
 CATTTGCTTA CTGACAGCAT TTTTGTAAA ACTGTTATTG TTGAAAAAAA AAAAAAAAAA 2640  
 AA

Seq ID NO: 56 Protein sequence;

Protein Accession #: AAC39582.1

1 11 21 31 41 51  
 | | | | |  
 MTALDLFLTN QFSEALSYLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA 60  
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEHAEVCY AECLLQRAAL TFLQDENMVS 120  
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSLMLPTIRLR 180  
 LLEFVGFSGN KDYGILLQLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGTG NVNIEBAEKL 240  
 LKPYLNRYPK GAIPLFFAGR IEVKGNDIA AIRRFEECE AQQHWKQFHH MCYWELMWCF 300  
 TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAVLSMFGK EDHKPFQDDE VELFRAVPGL 360  
 KLKIAAGSLP TEKFAIRKSR RYFSSNPISL PVALEMMYI WNGYAVIGKQ PKLTDGILEI 420  
 ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AHENFRSISA NEKKIKYDHY 480  
 LIPNALLELA LLLMBQDRNE EAIKLLESAK QNYKNYSMES RTHFRQAAT LQAKSSLENS 540  
 SRSMVSSVSL

Seq ID NO: 57 DNA sequence

Nucleic Acid Accession #: NM\_006670.1

Coding sequence: 1-927 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGCTGGGG GGTGCTCCG GGGCCCCGCC GCCGGGGACG GCGTCTGCG GCTGGCGCGA 60  
 CTAGCGCTGG TACTCCTGGG CTGGGCTCC TCGTCTTCTC CCACCTCTC GGCATCCTCC 120  
 TTCTCTCTCT CGGCGCGGTT CTTGGCTTCC GCGTGTCCG CCCAGCCCCC GCTGCCGGAC 180  
 CAGTCCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACC GC 240  
 AATCTGACCG AGGTGCCAC GGAACCTGCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300  
 AACCAGCTGG CCAGCAACCA CTCTCTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360  
 AGCCTCAGGC ACCTGGAATT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTTTC 420  
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480  
 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACAITA GGGTTTCTCT GGACAACAAT 540  
 CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600  
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAG AAATGAGGAA TCGGGTCTCT 660  
 TTGGAACCTA ACAGTGTGTA CCTGGAAGT GACCCGATTC TCCCCCATC CCTGCAAAACC 720  
 TCTATGTCT TCTGGGTAT TGTTTAGCC CTGATAGGCG CTATTTTCTT CTGGTTTGTG 780  
 TATTGAAAC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840  
 CACATGGAAG GGTATCAITA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900  
 AGTTCTAACT CGGATGTCTT CGAGTGA

Seq ID NO: 58 Protein sequence

Protein Accession #: NP\_006661.1

1 11 21 31 41 51  
 | | | | |  
 MPGGCSRGA AGDGLRLAR LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPLPD 60  
 QCPALCECE AARTVKVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLQALP 120  
 SLRHLDSNN SLVSLTVSF RNLTHTLESL LEDNALKVLH NGTLAELQGL PHIRVFLDNN 180  
 PWVCDCHMAD MVTLWKETEV VQGDRLTCA YPEKMRNRVL LELNSADLDC DPILPPLQT 240  
 SYVFLGIVLA LIGAFLLVL YLNRKGKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300  
 SSNSDVLE

Seq ID NO: 59 DNA sequence

Nucleic Acid Accession #: NM\_024022



Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

```

1   11   21   31   41   51
|   |   |   |   |
5  ATGGGGGGAAA ATGATCCGCC TGCTGTTGAA GCCCCCTTCT CATTCCGATC GCTTTTGGC 60
   CTGTGATGATT TGAAAATAAG TCCTGTTGCA CCAGATGCAG ATGCTGTTCG TGCACAGATC 120
   CTGTCACTGC TGCCATTGAA GTTTTTTCCA ATCATCGTCA TTGGGATCAT TGCATTGATA 180
   TTAGCACTGG CCATTTGGTCT GGGCATCCAC TTCGACTGCT CAGGGAAGTA CAGATGTCCG 240
   TCATCCTTTA AGTGTATCGA GCTGATAGCT CGATGTGACG GAGTCTCGGA TTGCAAAGAC 300
10  GGGGAGGACG AGTACCGCTG TGTCCGGGTG GGTGGTCAGA ATGCCGTGCT CCAGGTGTTC 360
   ACAGCTGCTT CGTGGGAAGAC CATGTGCTCC GATGACTGGA AGGGTCACTA CGCAAATGTT 420
   GCCTGTGCCC AACTGGGTTT CCAAGCTAT GTGAGTTCAG ATAACCTCAG AGTGAGCTCG 480
   CTGGAGGGGC AGTTCGGGGA GGAGTTTGTG TCCATCGATC ACCTCTTGCC AGATGACAAG 540
   GTGACTGCAT TACACCACTC AGTATATGTG AGGGAGGGAT GTGCCCTCTGG CCACGTGGTT 600
15  ACCTTGCACT GCACAGCCTG TGGTCATAGA AGGGGCTACA GCTCAGGCAT CGTGGGTGGA 660
   AACATGTCTT TGCTCTCGCA GTGGCCCTGG CAGGCCAGCC TTCAGTTCCA GGGCTACCAC 720
   CTGTGCGGGG GCTCTGTCT CACGCCCTG TGGATCATCA CTGCTGCACA CTGTGTTTAT 780
   GACTGTGACC TCCCAAGTTC ATGGACCATC CAGGTGGGTC TAGTTTCCCT GTTGGACAAT 840
   CCAGCCCCAT CCCACTTGGT GGAGAAGATT GTCTACCACA GCAAGTACAA GCCAAAGAGG 900
20  CTGGGCAATG ACATCGCCCT TATGAAGCTG GCCGGGCCAC TCAGTTCAA TGAAATGATC 960
   CAGCCTGTGT GCTGCCCCAA CTCTGAAGAG AACTTCCCGG ATGGAAAAAGT GTGCTGGACG 1020
   TCAGGATGGG GGGCCACAGA GATGAGAGGT GACGCCCTCC CTGTCTGAA CCACGCGGCC 1080
   TCCCTTTTGA TTCCAACAA GATCTGCAAC CACAGGGACG TGTACGGTGG CATCATCTCC 1140
   CCCTCCATGC TCTGCGCGGG CTACCTGACG GGTGGCGTGG ACAGCTGCCA GGGGGACAGC 1200
25  GGGGGGCCCC TGGTGTGTCA AGAGAGGAGG CTGTGGAAGT TAGTGGGAGC GACCAGCTTT 1260
   GGCATCGGCT GCGCAGAGGT GAACAAGCCT GGGGTGTACA CCCGTGTAC CTCCTTCTG 1320
   GACTGGATCC ACGAGCAGAT GGAGAGAGAC CTAAAAACCT GA

```

Seq ID NO: 60 Protein sequence

Protein Accession #: NP\_076927

```

1   11   21   31   41   51
|   |   |   |   |
35  MGENDPPAVE APFSFRSLFG LDDLKISVPA PDADAVAAQI LSLPLKFFP IIVIGHALI 60
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   TAASWKTMC SDDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
   VTALHHSYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
   LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300
40  LGNDIALMKL AGLPTNEMI QPVCLPNEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA 360
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Seq ID NO: 61 DNA sequence

Nucleic Acid Accession #: NM\_006475

Coding sequence: 28-2538 (underlined sequences correspond to start and stop codons)

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   ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
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   CAAATTTGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
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   TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTCCACGAG GTGTCTTAGA AAGGTTTCA 900
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Seq ID NO: 62 Protein sequence:

Protein Accession #: NP\_006466

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 40 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GREYTLAPVN NAFSDDTLIS 420  
 VQRLKLLIQ NHIKLVKVL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480  
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 FKGMTSEBK ILRDKNALQ NULYHLTPG VFIGKGFEPG VTNLKTTQG SKIFLKEVND 600  
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 45 TEVIHGEPII KKYTKIIDGV PVEITEKETR EERITGPFI KYTRISTGGG ETEETLKL 780  
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Seq ID NO: 63 DNA sequence

Nucleic Acid Accession #: NM\_020974

Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

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 65 GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
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 Protein Accession #: NP\_066025.1

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Seq ID NO: 66 Protein sequence:  
 Protein Accession #: NP\_009141

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Seq ID NO: 67 DNA sequence  
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55 Seq ID NO: 71 DNA sequence  
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 CCAATAAAG GCTTCTAAT GACAAAAATG GCATGTTTGC ATGATGAAAT GGAATGAAC 2640  
 AGTATTGCAA TGTCGGTAT ACAAAATAAC ATTAATTCAA TGTAGATAAA ATTACACTAG 2700  
 TTTAAATAT GTGCATTCAC TTGTATTGT TAGTGTTTA GTCITTTTTG AAAGATGTGC 2760  
 TCTGTTAATG TTGCTTTTT TTTTTTTT TAATACATGC TAGTCTAACA TTTCTGCTC 2820  
 TATGCCGCA TCTTTAACA TGCCAAAGT GAAGAAAAAT CTACCTTTTT TGTTAACAAG 2880  
 ACACGTACTT GAAACATGTA CATTTAAAGC CTTTATTTT TTCCCTTTT GTTTGGTAG 2940  
 TTGGGCATTT AAATAAGGAC AAGGAAAAAT ATTTTGGGG GCAATCAAG AGCCTATGAG 3000  
 TTCTAAGTAT AAAGCTGAAG TGATTTGGA TGCCAGCGTT ATATATTGTC ATTTTCACA 3060  
 TTTACGAGG GAGTATATGT GTATGTGTGT GCACGCATGC ATGTGTATGT GTTTGCTTT 3120  
 TTGTTTCCAT CACTAATCA AAAAGGATAA TTAGAAAAAT GGAGCATGAT GGGAAACAGA 3180  
 GTTTTGTACT TTAATAAACA GATGAGTTGT TTTTATAAGT AGACTCCACT GGGGTAGAGG 3240  
 TATTCACTTT AAAACATAGG GTGAGTAGAT GCTTTTITAG GCCTTTTGT GTATATGTAC 3300  
 GTTGTGTGTT TTTTCTTT TGTTCATAGC CTGTTCACTG TACAGTTTAT TCAAGGCTAC 3360  
 ATGCTTTTTT TTAATGCTC TGGCTATGCA TTTTCTTTT TTACATATAG GATTGGGAT 3420  
 TGGGGTGGG TTGGATGTT TTTTGGGG ACTTATTTAG TAGTATTGAG TCTCTTATAG 3480  
 CCTACTCTT AAGCCTCAA TACTGTCCAC TCTTATATT CCTTACTTG CAGAAITTTAT 3540  
 AAAAGCCCC AAACGTGATA TAATATGAGC CTTAAAAACA TGGTAAAAAC TAATCCCAT 3600  
 GATGGGTTTG GATGGTATGT TAAGAAATGG AGATGCTGCA GAGCCCAACG TAATTTTTTA 3660  
 AACAGCAAGT TTTCCATCTC CTTACGAATC CTCTGAAGCT TTAACCAAG CCCTTCTTG 3720  
 CCTCTCCAGT GCTATTTCC TFCAGATGGA CCTTAAACAT AATTCTTGG ACTACTAG 3780  
 AGAGACTTCG AGGCAATAAT AAAAGATCAG TATTAACCAAG CTATAACAGA GGTGTGATCA 3840  
 TGCTACTTG TACAGTTTT CCCCCTTTT AAAAGGAAT GTAATAAAT TGTTTTTTC 3900  
 CATAGAATTA AATAATATTA AATTGAGTG AAAGGTGAT TGTGTATGAA TAGAATAGTA 3960  
 CCTCTCATCT GTGCAGTGT TCAATTCACC TCAGAGAAAA GGATACATAA GAGGAGTTTG 4020  
 TAATTTATCT TAGGATATTC TAATTGCATT TAAAGAACT TATCTTGGC AGGGTAAATG 4080  
 GGGGACTCAC ATACATATAT TAATACCTCT GACTCATTA CAGAAAGAAA TACTTGGTAC 4140  
 TTTTTCGCT GAATGACCAT ACTGTGGAGG ATGCATACTA TTTGTATAG AGAAATAAAT 4200  
 GAGGAAGAAA GAACTGCTTA ATTAATATAT CATTCATATG TCCATATAGA GACCATCTGG 4260  
 TTGCCATGTG TATATGTGA CATACTTTT GAATAGTTAC ATATCACAAG TATGTAGTTC 4320  
 ATGTTTGTGT TGTGGGGTA AGGCATCAGG AAAAATGTAG TTAGTCTTT CTTAACTTAT 4380  
 ACCAAATTA CCAACTATAT TATAGGAAAT ATGTGAAAT AGTTCATTAG CTTATTTCAC 4440  
 TATTATGCAT TCACATGATA TTAACCGTA CACTCACATG TTAGAATGAA AAGAGCAGTA 4500  
 GTTATCTTAG ATTTAAAAA CATGGATATC TTCTTGAAT CCTCAAGAT TGAGGTAGAG 4560  
 AATAAGAGCA AATCATCTG GAAGTACCTT AAGGAAACAA ACAGCAGCAG ATATTAGGT 4620  
 TAAACTTATT TTCATAATG TTTAATAACT TTTGTATAAT CTTCTTGTCT ATTATGAGAG 4680  
 AGAATGTATA TATCAATAT GTGTAATGAT AAAATCTGAA TTGTAAAT TTTGTATATT 4740  
 GTTAAATTTG TAATTCTAAA TTGTATTCA AAAATGATTA TTTCTGATAT TGTTTTTATG 4800  
 TCACCCATGA TGAACACTGG ACTTTATATA TCTAACATA CAAGTATGAA CTATTCTATT 4860  
 TAAATTTT AATAGTTTT TCTTTTTTG GTGCCTATA TTGATTGGTC ATTTCTGCTG 4920  
 GCTTTTCTCC AATGAACATT GAAATCTTCT TGTATATGTT ACCAATAAGA AAACCTACCT 4980  
 GGAACAGTAG AAAAACCCAA CAAGAGACTT GGCATTTCAT AAGCACATTA TCAGACTTTG 5040  
 AGAACATATT GAAGGCATTG ACTTGAATA TCATCTCTT TCTCAAGAA GAAAGCAATG 5100  
 GAGAAGCAAA TTTGTTTCAT TCAGTGAATC CCCAGTTTGG GGCTTGTGGG GCTTAGAGAC 5160  
 ATTGTGAAAT CAAATCTTGT GTTATCTTT TCTCTGGCT CACTTTTTT GAGAAGGTTT 5220  
 ATGGGCTATT TGGCTGTGTA GACACGATCC CTTCTAAGA AAATGTAGGT GCTCAGACAG 5280  
 GTAACCACTG CTGCTACTGT TTTTATTGT TGTTTGTTT AATTTTATT AAGATTGTT 5340  
 TTTGTTGAT TAAATTTTA AAAAATGTAA TATATTGCAG GATTATAAC CAG

Seq ID NO: 72 Protein sequence  
 Protein Accession #: BAA86552

1 11 21 31 41 51  
 | | | | |



MCSSVAAKLW FLTDRIRED YPQKEILRAL KAKCCEBBLD FRAVVMDEVV LTIEQGNLGL 60  
 RINGELITAY PQVVVVVRYP PWVQSDSDIT VLRHLEKMG CRLMNRPOAIL NCVNKFWTFQ 120  
 ELAAGHGVPLP DTFSYGGHEN FAKMIDEAEV LEPPMVVKNT RGHROKAVFL ARDKHLADL 180  
 SHLIRHEAPY LFQKYVKESH GRDVRVIVVG GRVVGTM LRC STDGRMQSNC SLGGVGMMS 240  
 LSEQKQLAI QVSNILGMDV CGIDLLMKDD GSFVCEANA NVGFIAFDKA CNLDVAGHA 300  
 DYAAALLPSG RLTRRMSLS VVSTASETSE PELGPPASTA VDNMSASSSS VDSDEPSTER 360  
 ELLTKLPGL FNMNQLANE IKLLVD

Seq ID NO: 73 DNA sequence  
 Nucleic Acid Accession #: XM\_040080.2  
 Coding sequence: 159-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTGAGTGGGG GCGGGGACTG CTGGAGTTGC GGGGCTGCC TGGGGTAGGG CGGGGACGGA 60  
 CAGCTTGGAG ATAGGGCCCG GAATTGCGGG CGTCACTCTG CTCCTGCGAC CTAGCCAGGC 120  
 GTGAGGGAGT GACAGCAGCG CATTGCGGG ACGAGAGCGA TGAGTGAGAA CGCCGCACCA 180  
 GGTCTGATCT CAGAGCTGAA GCTGGCTGTG CCCTGGGGCC ACATCGCAGC CAAAGCCTGG 240  
 GGCTCCCTGC AGGGCCCTCC AGTTCTCTGC CTGCACGGCT GGCTGGACAA TGCCAGCTCC 300  
 TTGACACAGC TCATCCCTCT TCTCCCGCAA GACTTTTATT ACGTIGCCAT GGATTTCCGA 360  
 GGTCATGGGC TGGACACGCC GCTCTTCTC CTGGAATCAG ATGAAATGGA GAACTTGCTG 420  
 AGTGAGATCC GAAGAGTTGT GGCAGCCITG AATGGAATC GATTCTCCAT TCTGGGCCAC 480  
 AGCTTCGTG GCGTCGTGG CGGAATGTTT TTCTGTACCT TCCCGGAGAT GGTGGATAAA 540  
 CTATCTTGC TGGACACGCC GCTCTTCTC CTGGAATCAG ATGAAATGGA GAACTTGCTG 600  
 ACCTACAAGC GGAGAGCCAT AGAGCAGTG CTGCAGGTAG AGGCCTCCCA GGAGCCCTCG 660  
 CACGTGTTCA GCCTGAAGCA GCTGCTGCAG AGGTACTGA AGAGCAATAG CCAGTTGAGT 720  
 GAGGAGTGG GGGAGCTTCT CTTGCAAAAG GGAACACGA AGGTGGCCAC AGGTCTGGTT 780  
 CTGAACAGAG ACCAGAGGCT CCGCTGGCA GAGAACAGCA TTGACTTCAT CAGCAGGGAG 840  
 CTGTGTGGCG ATTCCATCAG GAAGCTGCAG GCCCATGTCC TGTGATCAA AGCAGTCCAC 900  
 GGATATTGTG ATCAAGACA GAATTACTCT GAGAAGGAGT CCCTGTGCTT CATGATAGAC 960  
 ACGATGAAAT CCACCTCAA AGAGCAGTTC CAGTTGTGG AAGTCCAGG CAATCACTGT 1020  
 GTCCACATGA GCGAACCCCA GCAGCTGGCC AGTATCATCA GTCCTTCTT ACAGTGCACA 1080  
 CACATGCTCC CAGCCAGCT GTAGCTCTGG GCCTGGAAC ATGAAGACCT AGTGCTCCCA 1140  
 GACTCAACAC TGGGACTCTG AGTTCCTGAG CCCACAACA AGGCCAGGGA TGGTGGGGAC 1200  
 AGGCCTCACT AGTCTTGAGG CCCAGCCTAG GATGGTAGTC AGGGGAAGGA GCGAGATTCC 1260  
 AACTTCAACA TCTGTGACCT CAAGGGGAG ACAGAGTCTG GGTCCAGGG CTGCTTCTC 1320  
 CTGGCTAATA ATAAATATCC AGCCAGCTGG AGGAAGGAAG GGCAGGCTGG GCCCACTAG 1380  
 CCTTCCCTG CTGCCCACT GGATGGAAAA TAAAGGTTT TGTATTCTC A

Seq ID NO: 74 Protein sequence:  
 Protein Accession #: XP\_040080.1

1 11 21 31 41 51  
 MSENAPGLI SELKLVWPWG HIAAKAWGSL QGPPVLCLHG WLDNASSFDR LIPLLPQDFY 60  
 YVAMDFGGHG LSSHYSPGVP YYLQTFVSEI RRVVAALKWN RFSILGHSFG GVVGGMFFCT 120  
 FPMEVDKLL LDTPLFLES DEMENLLTYK RRAIEHVLQV EASQEPHSVF SLKQLLRLL 180  
 KSNHLSEEC GELLQRGT KVATGLVLR DQLAWAENS IDPISRELCA HSIRKIQAHV 240  
 LLKAVHGYF DSRQNYSEKE SLSEFMIDTMK STLKEQFQFV EYPGNHCVHM SEPQHVASII 300  
 SSFLQCTHML PAQL

Seq ID NO: 75 DNA sequence  
 Nucleic Acid Accession #: NM\_005794  
 Coding sequence: 434-1276 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGTTCCTTC CAGCTGTGA AGCTTTGTTT TTTGGTCTT CATGATAAAT CTGCTGCTG 60  
 CTCACTGTT GGGTCCGTGC CACCTTAAG AGCTGTAACA CTCACCGCA AGGTCTGCAA 120  
 CTTCACTCT GGGGCCAGCA AGACCAGAA TGCACCGAGA GGAATGAACA ACTCTGGACA 180  
 CACCATCTT AAGAACCCTA ATACTACCG CAAGGGTCTG CAATTCATT CTTGAAGTCA 240  
 GTGAGGCCAA GAACCATCA ATTCCGTACA CATTTGGTG ACTTTGAAGA GACTGTACCC 300  
 TATCACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT 360  
 CACCAAGCGG TGAGACTATC ACCTATCGCC AAGTGGCCTG ATTCAGCAGG AAGCATCTCA 420  
 GACACCAACC ACTTGTGTGT CAGCAGTTGC CCGGGGCTAC CAGGCTGGT TTTATCCCTG 480  
 TGCTAGGCTT TCTGTAGGA TGAGCAGCAC CGGGATAGAC AGGAAGGGCG TCCTGGCTAA 540  
 CCGGGTAGCC GTGGTACCG GGTCCACCAG TGGGATCGGC TTTGCCATCG CCCGACGTCT 600  
 GGCCGGGGAC GGGGCCAGC TGGTCATCAG CAGCCGGAAG CAGCAGAAGC TGGACCGGGC 660  
 CATGGCCAAG CTGCAGGGGG AGGGGCTGAG TGTGGCGGGC ATTGTGTGCC ACGTGGGGAA 720  
 GGCTGAGGAC CGGGAGCAGC TGGTGGCCAA GGCCCTGGAG CACTGTGGGG GCGTCGACT 780  
 CCTGGTGTG AGCGCAGGGG TCAACCTCT GGTAGGGAGC ACTCTGGGGA CCAAGTGAGCA 840  
 GATCTGGGAC AAGATCTTAA GTGTGAACGT GAAGTCCCA GCCCTGCTGC TGAGCCAGTT 900  
 GCTGCCCTAC ATGGAGAACA GGAGGGGTGC TGTCTCTCTG GTCTCTTCCA TTGCAGCTTA 960  
 TAATCCAGTA GTGGCGCTGG GTGTCTACAA TGTACAGCAAG ACAGCGCTGC TGGGTCTCAC 1020  
 TAGAACACTG GCATTGGAGC TGGCCCCCAA GGACATCCGG GTAAACTGCG TGGTCCAGG 1080  
 AATTATAAAA ACTGACTTCA GCAAAGTGT TCAATGGGAAT GAGTCTCTCT GGAAGAACTT 1140  
 CAAGGAACAT CATCAGCTGC AGAGGATTGG GGAGTCAGAG GACTGTGCAG GAATCGTGTG 1200

CTTCTGTGC TCTCCAGATG CCAGCTACGT CAACGGGGGAG AACATTGCGG TGGCAGGCTA 1260  
 CTCCACTCGG CTCTGAGAGG AGTGGGGGCG GCTGCGTAGC TGTGGTCCCA GCCCAGGAGC 1320  
 CTGAGGGGGT GTCTAGGTGA TCATTGGAT CTGGAGCAGA GTCTGCCATT CTGCCAGACT 1380  
 AGCAATTGG GGGCTTACT ATGCTAGGCT TGAGGAAGAA GAAAAACGCT TCGGCATTCT 1440  
 CC

Seq ID NO: 76 Protein sequence:  
 Protein Accession #: NP\_005785

1 11 21 31 41 51  
 | | | | |  
 MLSAVARGYQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLRDQ 60  
 AHVVVSSRKQ QNVDRAMAKL QGEGLSVAGI VCHVGKABDR EQLVAKALEH CGGVDFLVCS 120  
 AGVNPVVGST LGTSEQIWDK ILSVNVKSPA LLSQLLPYM ENRRGAVILV SSIAAYNPVV 180  
 ALGVYNVSKT ALLGLTRTLA LELAPKDIRV NCVVPQIKT DFSKVFHGNE SLWKNFKEHH 240  
 QLQRIGESD CAGIVSFLCS PDASYVNGEN IAVAGYSTRL

Seq ID NO: 77 DNA sequence  
 Nucleic Acid Accession #: NM\_002425  
 Coding sequence: 26-1453 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCACTC CTGTGCTGT TGTGTCTGCC 60  
 AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120  
 TGCCAGCAAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180  
 AAAGGACAGT AATCTCATG TTAATAAAAT CCAAGGAATG CAGAAGTTC TTGGGTGGA 240  
 GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300  
 TCCTGACGTT GGTCACTTCA GCTCCTTTC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360  
 TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTG ATTCTGCCAT 420  
 TGAGAAAGCT CTGAAAGTCT GGAAGAGGT GACTCCACTC ACATTCCTCA GGCTGTATGA 480  
 AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540  
 TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600  
 TATTCACITT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT 660  
 CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACATGAAGC 720  
 TTTGATGTAC CCACCTTACA ACTCATTCAC AGAGCTCGCC CAGTTCGGCC TTTGCAAGA 780  
 TGATGTGAAT GGCATTGAGT CTCTCTACGG ACCTCCCTCT GCTCTACTG AGGAACCCCT 840  
 GGTGCCCAAA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900  
 GTCTCTGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960  
 TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTGTGGCC 1020  
 CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT 1080  
 TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140  
 AGGCATCCAT ACCCTGGGTT TTCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200  
 CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260  
 TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320  
 GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTCTTCA GTGGATCATC 1380  
 ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440  
 GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAT AAATCTAATA 1500  
 ATTATTCATC TAATGTATTA TGAAGCAAAA TGGTTAATTT TTCTGCGATG TTCTGTGACT 1560  
 GAAGAAGATG AGCCTTCCAG ATATCTGCAT GTGTATGAA GAATGTTCT GGAATCTTTC 1620  
 ACTTGCTTTT GAATTGCACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680  
 ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCTGTTC 1740  
 CTT

Seq ID NO: 78 Protein sequence:  
 Protein Accession #: NP\_002416

1 11 21 31 41 51  
 | | | | |  
 MHLAFLVLLC LPVCSAYPLS GAAKBEDSNK DLAQQYLEKY YNLEKIDVKQF RRKDSNLIVK 60  
 KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTYRIVNYT 120  
 PDLPRDAVDS AIEKALKVWE EVIPLTFSRL YEGEADIMIS FAVKEHGDYF SFDGPGHSLA 180  
 HAYPPGPGLY GDHFDDEK WTEDASG'NL FLVAHELGH SLGLFHSANT EALMYPLVNS 240  
 FTELAQFRLS QDDVNGIQLS YGPPFASTEB PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300  
 RGEVLFKDR YFWRSSHWNF EPEFHLSAF WPSLPVYLD AYEVSRTDV FIFKGNFWA 360  
 IRGNEVQAGY PRGIHTLGF PTIRKIDAAV SDKEKKKTYF FAADKYWRFD HNSQSMBQGF 420  
 PRLIADDFPG VEPKVDVAVLQ AFGFFYFFSG SSQFEFDPNA RMVTIBLXSN SWLHC

Seq ID NO: 79 DNA sequence  
 Nucleic Acid Accession #: NM\_000493.1  
 Coding sequence: 1-2043 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGCTGCCAC AAATACCCCT TTTGCTGCTA GTATCCTTGA ACTTGGTTCA TGGAGTGTTC 60  
 TACGCTGAAC GATACCAAC GCCCAGAGGC ATAAAGGCC CACTACCCAA CACCAAGACA 120

CAGTTCTTCA TTCCCTACAC CATAAAGAGT AAAGGTATAG CAGTAAGAGG AGAGCAAAGGT 180  
 ACTCCTGGTC CACCAGGCCG TGCTGGACCT CGAGGGCACC CAGGTCTTC TGGACCAACA 240  
 GGAACCAACG GCTACGGAAG TCCTGGACTC CAAGGAGAGC CAGGGTTGCC AGGACCACCG 300  
 GGACCATCAG CTGTAGGGA ACCAGGTGTG CCAGGACTCC CAGGAAAAAC AGGAGAGAGA 360  
 5 GGACCATATG GACCAAAAGG AGATGTTGGA CCAGCTGGCC TACCAGGACC CCGGGGCCCA 420  
 CCAGGACCAC CTGGAATCCC TGGACCGGCT GGAATTTCTG TGCCAGGAAA ACCTGGACAA 480  
 CAGGGACCCA CAGGAGCCCC AGGACCCAGG GGCITTCCTG GAGAAAAGGG TCCACCAGGA 540  
 GTCCCTGGTA TGAATGGACA GAAAGGGGAA ATGGGATATG GTGCTCCTGG TCGTCCAGGT 600  
 10 GAGAGGGGTC TTCCAGGCCG TCAGGGTCCC ACAGGACCAT CTGGCCCTCC TGGAGTGGGA 660  
 AAAAGAGGTG AAAATGGGGT TCCAGGACAG CCAGGCATCA AAGGTGATAG AGGTTTTCGG 720  
 GGAGAAATGG GACCAATTGG CCCACCAAGT CCCCAAGGCC CTCTGGGGA ACGAGGGCCA 780  
 GAAGGCATTG GAAAGCCAGG AGCTGCTGGA GCGCCAGGCC AGCCAGGGAT TCCAGGAACA 840  
 AAAGGTCTCC CTGGGGCTCC AGGAATAGCT GGGCCCCCAG GGCCTCCTGG CTTTGGGAAA 900  
 15 CCAGGCTTGC CAGGCCTGAA GGGAGAAAAG GGACCTGCTG GCCTTCCTGG GGGTCCAGGT 960  
 GCCAAAGGGG AACAAGGGCC AGCAGGTCTT CTTGGGAAGC CAGGTCTGAC TGGACCCCTC 1020  
 GGGAAATATG GACCCCAAGG ACCAAAAGGC ATCCCGGGTA GCCATGGTCT CCCAGGCCCT 1080  
 AAAGGTGAGA CAGGCCCAGC TGGGCTGCA GGATACCTGG GGGCTAAGGG TGAAAGGGGT 1140  
 TCCCTGGGT CAGATGGAAC ACCAGGCTAC CCAGGAAAAC CAGGTCTCGA TGGTCTTAAG 1200  
 20 GGTAAACCCAG GGTACCCAGG TCCAAAAGGT GATCCTGGAG TTGGAGGACC TCCTGGTCTC 1260  
 CCAGGCCCTG TGGGCCAGC AGGAGCAAGG GGAATGCCCG GACACAATGG AGAGGCTGGC 1320  
 CCAAGAGGTG CCCCTGGAAT ACCAGGTACT AGAGGCCCTA TTGGGCCACC AGGCATTCCA 1380  
 GGATTCCTCG GTCTTAAAGG GGATCCAGGA AGTCCCGGTC CTCCTGGCCC AGCTGGCATA 1440  
 GCAACTAAGG GCCTCAATGG ACCCACCAGG CCACCAAGGC CTCCAGGTCC AAGAGGCCCC 1500  
 25 TCTGGAGAGC CTGGTCTTCC AGGGCCCCCT GGGCTCCAG GCCCACCAGG TCAAGCAGTC 1560  
 ATGCCCTGAGG GTTTTATAAA GGCAGGCCAA AGGCCCAGTC TTTCTGGAC CCTCTTGT 1620  
 AGTGCCAACC AGGGGGTAA AGGAATGCCT GTGTCTGCTT TACTGTAT TCTCTCCAAA 1680  
 GCTTACCCAG CAATAGGAAC TCCATACCA TTGATAAAA TTTGTATAA CAGGCAACAG 1740  
 CATTATGACC CAAGGACTGG AATCTTACT TGTACAGATC CAGGAATATA CTATTTTCA 1800  
 30 TACCAGTGC ATGTGAAAGG GACTCATGTT TGGGTAGGCC TGTATAAGAA TGGCACCCTC 1860  
 GTAATGTAGA CTTATGAATG ATACACAAA GGCTACCTGG ATCAGGCTTC AGGGAGTGCC 1920  
 ATCATCGATC TCACAGAAAA TGACCAGGTG TGGCTCCAGC TTCCCAATGC CGAGTCAAA 1980  
 GGCCTATACT CCTCTGAGTA TGTCCACTCC TCTTCTCAG GATTCCTAGT GGCTCCAATG 2040  
 TGAGTACACC CCACAGAGCT AATCTAAATC TTGTGCTAGA AAAAGCATTC TCTAACTCTA 2100  
 35 CCCCACCCTA CAAAATGCAT ATGGAGGTAG GCTGAAAAGA ATGTAATTTT TATTTCTGA 2160  
 AATACAGATT TGAGCTATCA GACCAACAAA CCTTCCCCCT GAAAAGTGAG CAGCAACGTA 2220  
 AAAACGTATG TGAAGCCTCT CTGGAATTTC TAGTTAGCAA TCCTAAGGCT CTTAAGGTT 2280  
 TTCTCCAATA TTAATAAATA TCACCAAGA AGTCTGCTA TGTTAAAAAC AAACAACAAA 2340  
 AAACAAAGCA ACAAAAAAAA AAATAAAAAA AAAAAACAGA AATAGAGCTC TAACTATGT 2400  
 40 GAAATTGTAT TTGAGAAACT CGGCATTICC TTTTAAAAA AGCCTGTTTC TAACATGAA 2460  
 TATGAGAACT TCTAGGAAAC ATCCAGGAGG TATCATATAA CTTGTAGAA CTAAATACT 2520  
 TGAATATTCA AATTAAAAAG ACACGTATC CCTAAAAATA TTTCTGATGG TCACTACTC 2580  
 TGAGGCTGT ATGGCCCTT TCATCAATAT CTATTCAAAT ATACAGGTGC ATATATACT 2640  
 GTTAAAGCTC TTATATAAAA AAGCCCAAAA ATATTGAAGT TCATCTGAAA TGCAAGGTGC 2700  
 45 TTTTATCAAT GAACCTTTT AAAACTTTT TATGATTGCA GAGAAGCTTT TTATATACC 2760  
 AGCATAACTT GGAAACAGGT ATCTGACCTA TCTTATTTA GTTAACACAA GTGTGATTAA 2820  
 TTTGATTCTT TTAATTCCTT ATTGAATCIT ATGTGATATG ATTTCTGGA TTACAGAAC 2880  
 ATTAGCACAT GTACCTTGTG CCTCCATTTC AAGTGAAGTT ATAATTIACA CTGAGGGTTT 2940  
 CAAAATTGCA CTAGAAGTGG AGATATATTA TTATTTATG CACTGTACTG TATTTTATA 3000  
 50 TIGCTGTTTA AAACTTTTAA GCTGTGCTC ACTTATTTAA GCACAAAATG TTTTACCTAC 3060  
 TCCTTATTTA CGACACAATA AAATAACATC AATAGATTTT TAGGCTGAAT TAATTGAAA 3120  
 GCAGCAATTG GCTGTCTCA ACCATCTTT CAAGGCTTTT CATTGACAC AATAAAATAA 3180  
 CATCAATAGA TTTTAGG

Seq ID NO: 80 Protein sequence:

Protein Accession #: NP\_000484.1

1 11 21 31 41 51  
 | | | | |  
 60 MLPQIPFLL VSLNLVHGVF YAERYQPTG IKGPLNTKT QFFIPYTIKS KGIIVRGEQG 60  
 TPQPPGAPG RGHGPGSGPP GKPGYSGPL QGEPGLPGP GPSAVGKPGV PGLPGKPGER 120  
 GPYGPKGDVG PAGLPGRGP PGPPGPGPA GISVPGKPGQ QGPTGAPGR GFPGKGPAG 180  
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKGDRGFP 240  
 65 GEMGPPIPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300  
 PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQPGK IPGSHGLPGP 360  
 KQETGPAPGA GYPGAKGERG SPGSDGKPGY PGKPLDGPK GNPGLPGPKG DPGVGGPPGL 420  
 PGPVGPAGAK GMPGHNGEAG PRGAPGPGT RGPPIPPGP GPPGSKGDPG SPGPPGPA 480  
 ATKGLNGPTG PPGPPGPRGP SGEPGLPGPP GPPGPPQAV MPEGFIKAGQ RPSLSGTPLV 540  
 70 SANQGVGMP VSAFTVLSK AYPAGTTP FDKILYNRQ HYDPRTGIFT CQPGIYYS 600  
 YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IDLTENDQV WLQLPNAESN 660  
 GLYSSEYVHS SFGFLVAPM

Seq ID NO: 81 DNA sequence

Nucleic Acid Accession #: NM\_000786

Coding sequence: 332-1861 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5 CGCGATTCTC AGGGATTGAT CCGCCTCTTC AGGTAAGTTA TCTCCGGGCC CCGTACCACT 60  
 GTGCCACAGG CGCAGCCCCG TTCCTCAGGT GCCCTATCCC GCGCAGAAAG CCACGGCTTC 120  
 ACAGAGTGT ATTAAAGGCG GTGGCCAGCG GAACATCCCC CCCCATTTCTG TGACGCACGG 180  
 GGTGGCGCG GTGGGACCCG AGGGGTGGGG CTGGGTTTAG TAGGAGACCT GGGGCAAGGC 240  
 CCCCCTGTGA CGACCATCTG CCAGCTTCTC TCGTCCGTC GATTGGGAGG AGCGGTGGCG 300  
 ACCTCGGCCT TCAGTGTTC CGACGGAGTG AATGGCGCG GCGGCTGGGA TGCTGCTGCT 360  
 GGGCTTGCTG CAGGCGGGTG GGTGCGTGCT GGGCCAGGCG ATGGACAAGG TGACAGGCGG 420  
 CAACCTCTTG TCCATGTGTC TGATCGCCTG CGCCTTCACC CTCAGCCTGG TCTACCTGAT 480  
 10 CCGTCTGGCC GCCGCCACC TGGTCCAGCT GCCCGCAGGG GTGAAAAGTC CTCCATACAT 540  
 TTTCTCCCA ATTCATTCC TTGGGCATGC CATAGCATTI GGGAAAAGTC CAATTGAATT 600  
 TCTAGAAAAT GCATATGAGA AGTATGGACC TGTATTAGT TTTACCATGG TAGGCAAGAC 660  
 ATTTACITAC CTCTGGGA GTGATGCTGC TGCACTGCTT TTAATAGTA AAAATGAAGA 720  
 CCTGAATGCA GAAGATGTCT ACAGTCGCCT GACAACACCT GTGTTTGGGA AGGGAGTTGC 780  
 15 ATACGATGTG CCTAATCCAG TTTCTTGGG GCAGAAGAAA ATGTIAAAAA GTGGCCTTAA 840  
 CATAGCCAC TTTAAACAGC ATGTTCTAT AATTGAAAAA GAAACAAAGG AATACTTTGA 900  
 GAGTTGGGGA GAAAGTGGAG AAAAAAATGT GTTTGAAGCT CTTCGAGC TCATAATTTT 960  
 AACAGCTAGC CTTATTTGC ATGGAAAAGG AATCAGAAGT CAACTCAATG AAAAGGTAGC 1020  
 ACAGCTGTAT GCAGATTGG ATGGAGGTTT CAGCCATGCA GCCTGGCTCT TACCAGGTTG 1080  
 20 GCTGCCTTG CCTAGTTTCA GACGCAGGGA CAGAGCTCAT CGGAAAATCA AGGATATTTT 1140  
 CTATAAGGCA ATCCAGAAAC GCAGACAGTC TCAAGAAAAA ATTGATGACA TTCTCCAAAC 1200  
 TTTACTAGAT GCTACATACA AGGATGGGCG TCCITGACT GATGATGAAG TAGCAGGGAT 1260  
 GCTTATGGA TTACTCTTG CAGGGCAGCA TACATCTCA ACTACTAGTG CTGGATGGG 1320  
 25 CTCTTTTGT GCCAGAGACA AAACACTTCA AAAAAAATGT TATTAGAAC AGAAAACAGT 1380  
 CTGTGGAGAG AATCTGCCTC CTTTAACTTA TGACCAGCTC AAGGATCTAA ATTTACTTGA 1440  
 TCGCTGTATA AAGAAACAT TAAGACTTAG ACCTCCTATA ATGATCATGA TGAGAATGGC 1500  
 CAGAACTCCT CAGACTGTGG CAGGGTATAC CATTGCTCCA GGACATCAGG TGTGTGTTTC 1560  
 TCCCACTGTC AATCAAGAC TTAAGACTC ATGGGTAGAA CGCCTGGACT TTAATCTTGA 1620  
 30 TCGTACTTA CAGGATAACC CAGCATCAGG GGAAGAGTTT GCCTATGTGC CATTGGAGC 1680  
 TGGGCGTCA CTGTGTATG GGGAAAATTT TGCCTATGTT CAAATTAAGA CAATTTGGTC 1740  
 CACTATGCTT CGTTTATATG AATTGTATCT CATTGATGGA TACTTTCCCA CTGTGAATTA 1800  
 TACAACATAG ATTCACACCC CTGAGAACC AGTTATCCGT TACAAACGAA GATCAAAATG 1860  
 AAAAAAGTTG CAAGGAACGA ATATATGTGA TTATCACTGT AAGCCACAAA GGCATTTCGA 1920  
 35 GAGAATGAAG TGTACAAAAC AACTCTGTGA GTTTACTGTT TTTTAAAGTG TGTAATCTTA 1980  
 AAAGCCAGTT TATGATTAG GATTGTGTA ACTGAATGGT TCTATCAAA ATAATAGCAT 2040  
 TTGACACATT TTCTAATAGT TATGATACTT ATACATGTGC TTCAGGAAG TTCCTTGGTG 2100  
 AAACAATGTG TGAGGGGGGA TCTAGGTAAT TGGCAGATTC TAAATAATAT AATTTCAGG 2160  
 TAGTAATTTT AAGAGTACT CTGCTCTTG CCAATAAAGT TCAGGGTATT CAAATCTTGG 2220  
 40 ACTAGTCTG CAAGGTATAA AGAATAAAAA TCCCAGTGAG ATACTTGGAA ACCACAGTTT 2280  
 ATTATTATTT ATCTGGGCAA TTATGTGTG TGTGAGGATG GAAGGGTAGG GAATAATCGA 2340  
 ACATCTAAAG CCTTGAATTA GAGAATACTA ATGTGTTTGG TATGATGATA CTCAGAAATG 2400  
 GAGATATTAT AGGAAAAAGA AATCCTTGG AATTTAAC TAAATCACTG CATATGGGAA 2460  
 ATTAAGAGAT CCAGGACCAT ATTTGATAAG AGTTCCTAAA AATAATGTAA TTATTAATGC 2520  
 TAAAGACTGC TCATGTATCT TGATCTAATT ACTAAATAAA TTACATATTT ATTTACCTGA 2580  
 45 TAAATATGTA TCTAGTTCTA CAAGGTACA TTTATGTGA AGTCCAAAGT CAAGTCCTTA 2640  
 GGGGATAATT TTGTTTGGG CTCAGTTGTT CCTGCTTCC TTTTITTTT TTTTITTTT 2700  
 TTGAGATGGA GTCTGCTCT GTTGCCAGG CTGGAGTGCA GTGTTGCGAT CTCAGCTCAC 2760  
 TGCATCCTCT GCTCCCGGG TTCAAGCAAT TCTCTGCTC AGCCTCCAA GTAGTTGGGA 2820  
 50 TTACAGGCAC CTGCCACCAT GCCTGGCTAA TTTTGTGAT TTTTAGTAGA GACGGGGGT 2880  
 TCACATGTTT GGCTAGGCTG GTCTTGAAC CTGAGCCTC GTGAGTCCAC CCGCTTGGC 2940  
 CTCCCAAAGT GCTGGGATTA CAGGCATGAG CCACCGCACC TGGCTTCCC TGCTTCTCT 3000  
 CTAGAATCCA ATTAGGGATG TTTGTTACTA CTCATATTGA TTAACACAGT TAACAACTT 3060  
 TTTTCTTTT AAAATGTGAG ATCAGTGAAC TCTGGTTTA AGATAATCTG AAACAAGGTC 3120  
 55 CTGGGAGTA ATAAATTTGG TCACATTCTG TAAAGCATAT TCTGTTAGG AATCAACTTA 3180  
 TCTCAATTTG TAACCTGGGG CCTAACTATA TGAGATGGCT GAAAAATAC CACATCGTCT 3240  
 GTTTTCACTA GGTGATGCCA AAATATTTTG CTTTATGTAT ATTACAGTTC TTTTAAAAAC 3300  
 ACTGGAAGAC TCATGTTAAA CTCTAATTGT GAAGGCAGAA TCTCTGTAA TTTTCAGAT 3360  
 TAAAAATCTC TTTGAAAAAA T

Seq ID NO: 82 Protein sequence:  
 Protein Accession #: NP\_009777

1 11 21 31 41 51  
 65 MAAAAGMLLL GLLQAGGSVL GQAMEKVTGG NLLSMLLIAC AFTLSLVYLI RLAAGHLVQL 60  
 PAGVKSPFY FSPFPLGHA IAPGKSPIEF LENAYERYGP VFSFTMVGKT FTYLLGSDAA 120  
 ALLFNSKND LNAEDVYSRL TTPVFGKGA YDVPNPVLE QKKMLKSLN IAHFKQHSI 180  
 IEKETKEYFE SWGESGEKNV FEALSELIL TASHCLHGKE IRSQLNEKVA QLYADLDGGF 240  
 70 SHAAWLLPGW LPLPSFRRRD RAHREIKDI YKAIQKRRQS QEKIDDLQT LLDATYKDGR 300  
 PLTDDEVAGM LIGLLAGQH TSSTSAWMG FFLARDKILQ KCCYLEQKTV CGENLPLTY 360  
 DQLKDLNLLD RCIKETLRLR PPIIMMRMA RTPQTVAGYT IPPGHQVCVS PTVNQRLKDS 420  
 WVERLDNFND RYLQDNFASG EKFAFVFPFA GRHRCIGENF AYYQKTIWS TMLRIYFDL 480  
 IDGYFTVNY TMIHTPENP VIRYKRRSK

Seq ID NO: 83 DNA sequence  
 Nucleic Acid Accession #: NM\_006551.2  
 Coding sequence: 64-336 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | |  
AATTCTAGAA GTCCAAATCA CTCATTGTTT GTGAAAGCTG AGCTCACAGC AAAACAAGCC 60  
5 ACCATGAAGC TGTCGGTGTG TCTCTGCTG GTCACGCTGG CCTCTGCTG CTACCAGGCC 120  
AATGCCGAGT TCTGCCAGC TCTGTTTCT GAGCTGTTAG ACTTCTTCT CATTAGTGAA 180  
CCTCTGTTCA AGTTAAGTCT TGCCAAATTT GATGCCCTC CGGAAGCTGT TGCAGCCAAG 240  
TAGGAGTGTA AGAGATGCAC GGATCAGATG TCCCTTCAGA AACGAAGCCT CATTGCGGAA 300  
10 GTCCTGGTGA AAATATTGAA GAAATGTAGT GTGTGACATG TAAAACTTT CATCTGGTT 360  
TCCACTGTCT TTCAATGACA CCTGATCTT CACTGCAGAA TGTAAGGTT TCAACGTTCT 420  
GCTTTAATAA ATCACTTGCT CTAC

Seq ID NO: 84 Protein sequence:

Protein Accession #: NP\_006542.1

1 11 21 31 41 51  
| | | | |  
MKLSVCLLLV TLALCCYQAN AEFCPALVSE LLDDFFISEP LFKLSLAKFD APPEAVAACL 60  
20 GVKRCTDQMS LQKRSLIAEV LVKILKKCSV

Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: NM\_002317.1

Coding sequence: 231-1484 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | |  
GGGCCAGGAC TGAGAAAGGG GAAAGGGAAG GGTGCCACGT CCGAGCAGCC GCCTTGACTG 60  
GGGAAGGGTC TGAATCCAC CCTTGGCATT GCTTGGTGGA GACTGAGATA CCCGTGCTCC 120  
30 GCTCGCTCC TTGGTTGAAG ATTCTCCTT CCTTCACGTG ATTTGAGCCC CGTTTTTATT 180  
TCTGTGAGC CACGTCTCC TCGAGCGGGG TCAATCTGGC AAAAGGAGTG ATGCGCTTCG 240  
CCTGGACCGT GCTCTGCTC GGGCCTTTC AGCTCTGCGC GCTAGTGAC TCGCCCTC 300  
CCGCCGCGG CCAACAGCAG CCCCCGCGG AGCCGCGGC GGTCTCCGGC GCCTGGCGCC 360  
AGCAGATCCA ATGGGAGAAC AACGGGCAGG TGTTCACTT GCTGAGCCTG GGCTCACAGT 420  
ACCAGCTCA GCGCCGCCG GACCCGGCG CCGCCGTCC TGGTGACGCC AACGCCTCCG 480  
35 CCCAGCAGC CCGCACTCC ATCTGTGTA TCCGCGACAA CCGCACC GCCGGGCGAA 540  
CGCGGACGGC CGGCTCATCT GGAGTCACCG CTGGCCGCC CAGGCCACC GCCCGTCACT 608  
GGTTCCAAGC TGGTACTCG ACATCTAGAG CCGCGAAGC TGGGCCCTCG CGCGCGGAGA 668  
ACCAGACAGC GCCGGGAGAA GTTCTGCTC TCAGTAACT GCGGCCGCC AGCCGCGTGG 720  
ACGGCATGGT GGGCGACGAC CCTTACAACC CCTACAAGTA CTCTGACGAC AACCTTATT 780  
40 ACAACTACTA CGATACTTAT GAAAGGCCCA GACCTGGGG CAGGTACCG CCGGATACG 840  
GCACTGGCTA CTTCAGTAC GGTCTCCAG ACCTGGTGGC CGACCCTAC TACATCCAG 900  
CGTCCACGTA CGTGACAGA AGTGTCCATGT ACAACCTGAG ATGCGCGCG GAGGAAAAC 960  
GTCTGGCCAG TACAGCATAC AGGGCAGATG TCAGAGATTA TGATCACAGG GTGCTGCTCA 1020  
45 GATTTCCTCA AAGAGTGAAA AACCAAGGGA CATCAGATT CTACCCAGC CGACCAAGAT 1080  
ATTCTGGGA ATGGCACAGT TGTCATCAAC ATTACCACAG TATGGATGAG TTTAGCCACT 1140  
TGTAACCTGT TGAATGCAAC ACCAGAGGA GATGGCTGA AGGCCACAAA GCAAGTTTCT 1200  
GTCITGAAGA CACATCCTGT GACTATGGCT ACCACAGCG ATTTGCATGT ACTGCACACA 1260  
CACAGGGATT GAGTCTGGC TGTATGATA CCTATGGTGC AGACATAGAC TGCCAGTGG 1320  
50 TTGATATTAC AGATGTAAAA CCTGGAACCT ATATCCTAAA GGTCAGTGA AACCCAGCT 1380  
ACCTGGTCC TGAATCTGAC TATACCAACA ATGTTGTGCG CTGTGACATT CGTACACAG 1440  
GACATCATGC GTATGCCCA GGCTGCACAA TTTCACCGTA TTAGAAGGCA AAGCAAACT 1500  
CCCAATGGAT AAATCAGTGC CTGGTGTCT GAAGTGGGA AAAATAGACT AACTTCAGTA 1560  
GGATTATGT ATTTTGAAAA AGAGAACAGA AAACAACAAA AGAATTTTG TTTGGACTGT 1620  
55 TTTCAATAAC AAAGCACATA ACTGGATTTT GAACGCTTAA GTCATCATT CTGGGAAAT 1680  
TTTAAATGTT TATATTTAC ATCACTTTGT GAATTAACAC AGTGTTCAA TTCTGTAATT 1740  
ACATATTTGA CTCITTCAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 86 Protein sequence:

Protein Accession #: NP\_002308.1

1 11 21 31 41 51  
| | | | |  
MRFAWTVLLI GPLQICLVH CAPPAAGQQQ PPPEPPAAPG AWRQQIQWEN NGQVFSLLSL 60  
GSQYQQRRR DPGAAPVPA NASAQPRTP ILLIRDNRTA AGRTRTAGSS GVTAGRPRPT 120  
65 ARHWFAQYS TSRAREAGPS RAENQTAPGE VPALSNLRPF SRVDGMVGDD PYNPKYSDD 180  
NPYYNYDDTY ERPRFGGRYR PGYGTGYFQY GLPDLVADPY YQASTYVQK MSMYNLRCAA 240  
BENCLASTAY RADVRDYDHR VLLRFPQVRK NQGTSDFLPS RPRYSWEWHS CHQHYHSMDE 300  
FSLYLLDAN TQRWAEGBHK ASFCLEDTSC DYGYHRRFAC TAHTQGLSPG CYDTYGADID 360  
70 CQWIDITDVK PGNYHLKVSV NPSYLVPESD YTNVVRCDI RYTGHHAYAS GCTISPY

Seq ID NO: 87 DNA sequence

Nucleic Acid Accession #: NM\_006419.1

Coding sequence: 91-420 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | |  
TTCGGCACTT GGGAGAAGAT GTTTGAAAA ACTGACTCTG CTAATGAGCC TGGACTCAGA 60

GCTCAAGTCT GAACTCTACC TCCAGACAGA ATGAAGTTCA TCTCGACATC TCTGCTTCTC 120  
 ATGCTGCTGG TCAGCAGCCT CTCTCCAGTC CAAGGTGTTT TGGAGGTCTA TTACACAAGC 180  
 TTGAGGTGTA GATGTGTCCA AGAGAGCTCA GTCTTTATCC CTAGACGCTT CATGTATCGA 240  
 ATTCAAATCT TCCCCCGTGG GAATGGTTGT CCAAGAAAAG AAATCATAGT CTGGAAGAAG 300  
 AACAAGTCAA TTGTGTGTGT GGACCCCTCA GCTGAATGGA TACAAAGAAT GATGGAAGTA 360  
 TTGAGAAAAA GAAGTTCTTC AACTCTACCA GTTCCAGTGT TTAAGAGAAA GATTCCCTGA 420  
 TGCTGATATT TCCACTAAGA ACACCTGCAT TCTTCCCTTA TCCCTGCTCT GGATTTTAGT 480  
 TTTGTGCTTA GTTAAATCTT TTCCAGGGAG AAAGAACTTC CCCATACAAA TAAGGCATGA 540  
 GGACTATGTG AAAAATAACC TTGCAGGAGC TGATGGGGCA AACTCAAGCT TCTTCACTCA 600  
 CAGCACCTTA TATACACTTG GAGTTTGCAT TCTTATTCAT CAGGGAGGAA AGTTTCTTGT 660  
 AAAATAGTTA TTCAGTTATA AGTAATACAG GATTATTTTG ATTATATACT TGTGTGTTAA 720  
 TGTTTAAAT TTCTTAGAAA ACAATGGAAT GAGAATTAA GCCTCAAAT TGAACATGTG 780  
 GCTTGAATTA AGAAGAAAAT TATGGCATAT ATTAAAAAGCA GGCTTCTATG AAAGACTCAA 840  
 AAAGTGCCT GGGAGGCGA TGGAACCTGA GCCTGTCAA AGGCAAGGA ATCCATGTAG 900  
 TAGATATCCT CTGCTTAAAA ACTCACTACG GAGGAGAAAT AAGTCTACT TTTAAAGAAT 960  
 TTCTTTATAA AATTTACTGT CTAAGATTAA TAGCATTGCA AGATCCCCAG ACTTCATAGA 1020  
 ATACTCAGGG AAAGCATTAA AAGGGTGAAT TACACATGTA TCCTTTCACA CATTTCCTT 1080  
 GACAAACCTT TTTCACCTAC ATCTTTTCA CTGACTTTT TTGTGGGGGC GGGGCCGGG 1140  
 GGACTCTGTT ATCTAATCT TTAATGATTC CTATAAATCT AATGACATTC AATAAAGTTG 1200  
 AGCAAACATT TTACTT

Seq ID NO: 88 Protein sequence:

Protein Accession #: NP\_005410.1

1 11 21 31 41 51  
 | | | | |  
 MKPISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFPRKPRFDR IQILPRNGNC 60  
 PRKEIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

Seq ID NO: 89 DNA sequence

Nucleic Acid Accession #: NM\_002652

Coding sequence: 37-477 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CTTCTCTGGG ACACATGGCT TTCTGTTTTC TCCAGCATGC GCTTGTCTCA GCTCCTGTTC 60  
 AGGGCCAGCC CTGCCACCTT GCTCCTGGTT CTCTGCCTGC AGTTGGGGGC CAACAAAGCT 120  
 CAGGACAACA CTCGGAAGAT CATAATAAAG AATTTTGACA TTCCCAAGTC AGTACGTCCA 180  
 AATGACGAAAG TCACCTGCAGT GCTTGCAGTT CAAACAGAAT TGAAAGAATG CATGGTGGTT 240  
 AAAACTTACC TCATTAGCAG CATCCCTCTA CAAGGTGCAT TTAACATATA GTATACTGCC 300  
 TGCCATGTG ACGACAATCC AAAACCTTC TACTGGGACT TTACACCAA CAGAACCTGTG 360  
 CAAATTGCAAG CCGTCGTTGA TGTATTTCGG GAATTAGGCA TCTGCCCTGA TGATGCTGCT 420  
 GTAATCCCCA TCAAAAACAA CCGGTTTTAT ACTATTGAAA TCTTAAAGGT AGAATAATGG 480  
 AAGCCCTGTC TGTTTGCCAC ACCCAGGTGA TTCCCTCTAA AGAAACTTGG CTGGAATTTT 540  
 TGCTGTGGTC TATAAAATAA ACTTCTTAAC ATGCTT

Seq ID NO: 90 Protein sequence:

Protein Accession #: NP\_002643.1

1 11 21 31 41 51  
 | | | | |  
 MRLQLLFRA SPATLLVL LQLGANKAQD NTRKHIKNF DIPKSVRPND EYTAVLAVQT 60  
 ELKECMVVKT YLISSIPQL AFNYKYTACL CDDNPKTFYW DFYTNRTVQI AAVVDVIREL 120  
 GICPDDAAVI PIKNRRFYTI EILKV

Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: AK000341

Coding sequence: 85-975 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GATAGCGCCG GGCAGAGGGA CCCGGCTACC CTGGACAGCG CATCGCCGCC CGCCCGGGTC 60  
 GCCCGGCCAC AGCCGCTGCG GATCATGGAA CATCTAAAGG CCTTTGATGA TGAAATCAAT 120  
 GCTTTTITGG ACAATATGTT TGGACCGCGA GATTCTCGAG TCAGAGGGTG GTTACGTTG 180  
 GACTCTTACC TTCTTACCTT TTCTTACT GTCATGTATC TGCTCTCAAT ATGGCTGGGT 240  
 AACAAGTATA TGAAGAACAG ACCTGCTCTT TCTCTCAGGG GTATCCTCAC CTGTGATAAT 300  
 CTTGGAATCA CACTTCTCTC CGCGTACATG CTGGCAGAGC TCATTCTCTC CACTTGGGAA 360  
 GGAGGCTACA ACTTACAGTG TCAAGATCTT ACCAGCGCAG GGAAGCTGA CATCCGGGTA 420  
 GCCAAGGTGC TTTGGTGGTA CTATTCTCC AAATCAGTAG AGTTCTTGA CACAATTTTC 480  
 TTCGTTTTGC GGAAGAAAAC GAGTCAGATT ACITTTCTTC ATGTATATCA TCATGCTTCT 540  
 ATGTTTAAAC TCTGGTGGTG TGCTTGAAC TGGATACCTT GTGGACAAAG TTTCTTTGGA 600  
 CCAACACTGA ACAGTTTGT CCACATCTT ATGTACTCCT ACTATGGACT TTCTGTGTTT 660  
 CCATCTATGC ACAAGTATCT TTGGTGAAG AAATATCTCA CACAGGCTCA GCTGGTGCAG 720  
 TFCGTGCTCA CCATCACGCA CACCATGAGC GCCGCTGTGA AACCGTGTGG CTCCCTCTTC 780  
 GGTGTCTTCA TCTTCCAGTC ATCTTATATG CTAACGTTAG TCATCTCTT CTTAAATTTT 840  
 TATGTTTGA CATACCGAAA AAAGCCAATG AAGAAAGATA TGCAAGAGCC ACCTGCAGGG 900  
 AAAGAAGTGA AGAATGGTTT TTCCAAGGCC TACTTCACTG CAGCAAATGG AGTGATGAAC 960

AAGAAAGCAC AATAAAATG AGTAACAGAA AAAGCACATA TACTAGCCTA ACAGATTGGC 1020  
 TTGTTTAAAA GCAAAGACTG AATTGAAGGT TACATGTTTT AGGATAAACT AATTCTTTTT 1080  
 GAGTTCATAA ATCAITTTGA CCCAGAATGT ATTAATATAT TGCTATTAGG TTAATCTGTT 1140  
 AACTGAATGC TTTGATCAGC ATTGAGGTGA TGCTCACCTC CGAGGACCTC AGAACTGGTG 1200  
 CAGCTTCTCT CTCCTCCCT CCCACAGACT GAACCTTCG CCAGAAGCTG TCCTTATAAC 1260  
 GCCTTATACG CATACACAGC CAGGAAACGT GGAGCATTGT TTCTACAGA GAGTCTCCAA 1320  
 ATAAAAAGGG TTTTGTTCAG ATTAATAATGT TTACAACAAA ATGTTAATTA TATTCTAAAT 1380  
 ACAGGTATG TTCTAATCTA TATTAAGCAA TAATGCCAGT GCATAATCAT TCCATTGTT 1440  
 CCTTTAGCAA TCAACCCAG AAAATATTAA AATGGGATCA TACACAGAAG ATAGAAAAAT 1500  
 CTAGCAAAAC TTCTCTTTCT GTAAGCCAGA GTCTTGCTA TCAGATTCCC ACAACCACTC 1560  
 CTGATTCTAA ATTAGTGAT ATGGTAATGA AATTGGTATT TATTTTAAAT ATTAGTTATT 1620  
 CTAAGGAGAA AAAATGCTT CTGCAAGATT TCCATAATC AGGGGCTGTG GATAGGATTG 1680  
 TTCTCTGTT TCCCTAATCA TTCATCTGTT CATGTCGCC TCTTGTCCTA GTCAGCTAG 1740  
 GTTATACAGA TGCCATGCTC CACACCAGA GCAGTGATCA AATCTGGCTG CCCGTTTACT 1800  
 TTCTGAGCAA GCACTGGAGT CCACTCCGAC CTTTTCTTT GAACATGCAT GCTGCTGGAA 1860  
 TATGTATAAA TCAGAAGTAG CAGAAGTAGC AGAGTGATGG GAGCAAAATA GGCAGTGAAT 1920  
 TCGTCAACTC TTTTGTGTA GCTTACTGT GAATATTACC TCAGATACTT GTTGTCACCT 1980  
 TTCAAGGTT ATTTAAGTTC TTGAAGCTGG GAGGAAAAAG ATGGAGTAGC TTGGAAGAT 2040  
 TCCAGCACTG AGCCGTGAGC CGGTGATGAG CCACGATAAA AAATGCCAGT TTGGCAAACT 2100  
 CAGCACTCCT GTTCCCTGCT CAGGTATATG CGATCTCTAC TGAGAAAGCAA GCACAAAAGT 2160  
 AGACCAAAGT ATTAATGAGT ATTTCTTTC TCCATAAGTG CAGGACTGTT ACTCACTACT 2220  
 AAACCTCTACC AAGAATGGAA ACCAAGAATA TTTTCTGAAG ATTTTGTGA AGATTAATTT 2280  
 ATACCCTATA AATAAAACT TGTAGCTTC GATGAAGTCA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 92 Protein sequence:  
 Protein Accession #: BAA91096.1

1 11 21 31 41 51  
 MEHLKAFDDE INAFLDNMFGRDRSRVRGWFLDSYLPFTFLVMYLLSIW LGNKYMKNRP 60  
 ALSLRGILTL YNLGITLLSA YMLAELILST WEGGYNLQCG DLTSAGEADI RVAKVLWVWY 120  
 FSKSVEFLDT IFFVLRRKTS QITPLHVYHH ASMFNIWVCV LNWIPOGQSF FGPTLNSFVH 180  
 ILMYSYYGLS VFPSMHKYLW WKKYLTAQL VQFVLTHTT MSADVVKPGF PFGCLIFQSS 240  
 YMLTLVILFL NFYVQTYRKK PMKKDMQEPF AGKEVKNGFS KAYFTAANGV MNKKAQ

Seq ID NO: 93 DNA sequence  
 Nucleic Acid Accession #: NM\_000044  
 Coding sequence: 1115-3874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGAGATCCCG GGGAGCCAGC TTGCTGGGAG AGCGGGACGG TCCGGAGCAA GCCACAGGC 60  
 AGAGGAGGCG ACAGAGGGAA AAAGGGCCGA GCTAGCCGCT CCAGTGTCTG ACAGGAGCCG 120  
 AAGGGACGCA CCACGCCAGC CCCAGCCCGG CTCAGCGAC AGCCAACGCC TCTTGACGG 180  
 CGGCGGCTTC GAAGCCGCGG CCGGAGCTG CCCTTTCTCT TTGGGTGAAG TTTTAAAAAG 240  
 CTGCTAAAGA CTCGGAGGAA GCAAGGAAAG TGCTGGTAG GACTGACGGC TGCTTTGTCT 300  
 CTCCTCTCTT CCACCCGCTT TCCCCCACC CTGCTCTCC CCCCCTCCC GTCTTCTCTC 360  
 CCGCAGCTGC CTCAGTCGGC TACTCTCAGC CAACCCCTT CACCACCTT CTCCCCACCC 420  
 GCCCCCCCCG CCCCCTCGCG CCAGCGCTGC CAGCCGAGT TTGCAGAGAG GTAATCCCT 480  
 TTGGCTGCGA GCGGGCGAGC TAGCTGCACA TTGCAAGAA GGCTCTTAGG AGCCAGGCGA 540  
 CTGGGGAGCG GCTTCAGCAC TGCAGCCACG ACCCGCTGG TTAGAATTCC GGCGGAGAGA 600  
 ACCCTCTGTT TTCCCCACT CTCTCTCCAC CTCTCTCTG CTCCCCACC CCGAGTGGG 660  
 AGCAGAGATC AAAAGATGAA AAGGCAGTCA GGTCTCAGT AGCCAAAAA CAAAACAAAC 720  
 AAAAAACAAA AAGCCGAAT AAAAGAAAA GATAATACT CAGTCTTAT TTGCACCTAC 780  
 TTCACTGGAC ACTGAATTG GAAGGTGGAG GATTTGTGTT TTTCTTTA AGATCTGGG 840  
 ATCTTTTGA TCTACCTTC AAGTATTAAG AGACAGACTG TGAGCCTAGC AGGGCAGATC 900  
 TTGTCCACCG TGTGTCTCT TCTGCACGAG ACTTTGAGGC TGTGAGAGCG CTTTGTGCT 960  
 GGTGTCTCCC GCAAGTTTCC TTCTCTGGAG CTCCCGCAG GTGGGCAGCT AGCTGCAGCG 1020  
 ACTACCGCAT CATCACAGCC TGTGAACTC TTCTGAGCAA GAGAAGGGGA GCGGGGGTAA 1080  
 GGGAAAGTAG TGGAAGATT AGCCAAGCTC AAGGATGAA GTGCAATTAG GGCTGGGAAG 1140  
 GGTCTACCTT CGGCGCGGT CCAAGACCTA CCGAGGAGCT TTCCAGAATC TGTTCAGAG 1200  
 CGTGGCGGAA GTGATCCAGA ACCCGGCGCC CAGGCACCCA GAGGCGCGA GCGCAGCACC 1260  
 TCCCGGCGCC AGTTTGCTGC TGCTGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA 1320  
 GCAGCAGCAG CAGCAGCAGC AGCAGCAAGA GACTAGCCCC AGGCAGCAGC AGCAGCAGCA 1380  
 GGGTGAGGAT GGTCTCTCCC AAGCCCATCG TAGAGGCCCC ACAGGCTACC TGGTCTGGA 1440  
 TGAGGAACAG CAACCTTCAC AGCCGAGTC GGCCCTGGAG TGCCACCCCG AGAGAGGTTG 1500  
 CGTCCAGAG CCGGAGCCG CCGTGCCGC CAGCAAGGGG CTGCCGAGC AGCTGCCAGC 1560  
 ACCTCCGGAC GAGGATGACT CAGTGCCTC CACTTCTCT TCCCTGCTGG GCGCCACTTT 1620  
 CCCCAGCTTA AGCAGCTGCT CCGCTGACCT TAAAGACATC CTGAGCGAGG CCAGCACCAT 1680  
 GCACTCTCT CAGCAACAGC AGCAGGAAGC AGTATCCGAA GGCAGCAGCA GCGGGAGAGC 1740  
 GAGGGAGGCT TCGGGGGCTC CCACTTCTC CAAGGACAAT TACTTAGGGG GCACTTCGAC 1800  
 CATTCTGAC AACGCCAAGG AGTTGTGTA GGCAGTGTG GTGTCCATGG GCCTGGGTGT 1860  
 GGAGGCGTTG GAGCATCTGA GTCCAGGGGA ACAGCTTCGG GGGGATTGCA TGTACGCCCC 1920  
 ACTTTTGGGA GTTCCACCCG CTGTGCTGCC CACTCTTGT GCCCATTTGG CCGAATGCAA 1980  
 AGGTCTCTG CTAGCAGCA GCGCAGGCAA GAGCACTGAA GATACTGCTG AGTATTCCCC 2040  
 TTCAAGGGA GGTACACCA AAGGCTAGA AGGCGAGAGC CTAGGCTGCT CTGGCAGCGC 2100  
 TGCAGCAGG AGCTCCGGGA CACTTGAAT GCCGTCTACC CTGTCTCTCT ACAAGTCCCG 2160

AGCACTGGAC GAGGCAGCTG CGTACCAGAG TCGCGACTAC TACAACITTC CACTGGCTCT 2220  
 GGCCGGACCG CCGCCCCCTC CGCCGCTCC CCATCCCCAC GCTCGCATCA AGCTGGAGAA 2280  
 CCCGCTGGAC TACGCGACCG CCTGGGCGCG TCGCGCGCGG CAGTGCCGCT ATGGGGACCT 2340  
 GCGGAGCCTG CATGGCGCGG GTGCAGCGGG ACCCGGTTCT GGATCACCTT CAGCCGCCCG 2400  
 TTCCTCATCC TGGCACACTC TCTTCACAGC CGAAGAAGGC CAGTTGTATG GACCGTGTGG 2460  
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 Protein Accession #: NP\_000035.1

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 Coding sequence: 135-1472 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 96 Protein sequence:

Protein Accession #: NP\_002488

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Seq ID NO: 97 DNA sequence

Nucleic Acid Accession #: NM\_007050.2

Coding sequence: 185-4576 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 98 Protein sequence:  
 Protein Accession #: NP\_008981.1

1 11 21 31 41 51  
 35 GIREFNPRO TEINTYROSI NEPHOSPHAT ASERECEPTO RYPETHOMO SAPIENSMAS 60  
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 MLDQAVPTGS FMMVNSSGRA SQQKAHLLP TLKENDTHCI DFHYFFSSRD RSSPGALNVY 180  
 VKVNGGPQGN PVWNVSGVVT EGWVKAELAI STFWPHFYQV IFESVSLKGH PGYIADDEV 240  
 40 VLAHPCRKAP HFLRLQNVVE NVGQNAITFC IAGGKWSQHD KLWLQQWNGR DIALMVTTRV 300  
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Seq ID NO: 99 DNA sequence  
 Nucleic Acid Accession #: NM\_002988.1  
 Coding sequence: 71-340 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 70 CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCCCTCGTCT ATACCTCCTG 180  
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 GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCCTGA GGGGCCTGGA AGCTGCGAGG 360  
 75 GCCCAGTGA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420  
 CCACCTGTGA GGCACCTCT TCTAAGAGTC CCATCTGCTA TGCCAGCCA CATTAACATA 480  
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 ATTATGAAAT TAGTATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTCCCT 600

TTCCCTTCAA CTCTTCGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCCTTCTCAG 660  
 CAGACATTGT GCCATATGTA TCAAATGACA AATCTTATAT GAATGGTTTT GCCTCAGCACC 720  
 ACCTTTTAAT ATATTGGCAG TACTTATTAT ATAAAAAGGTA AACCAGCATT CTCACGTGTA 780  
 AAAAAAAAAA AAAAAAAAAA AAA

Seq ID NO: 100 Protein sequence:  
 Protein Accession #: NP\_002979.1

1 11 21 31 41 51  
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 LLTKRGRQIC ADPNKKWVQK YISDLKINA

Seq ID NO: 101 DNA sequence  
 Nucleic Acid Accession #: NM\_015507.2  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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 GGGTCGGGCC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTCCGAGA 240  
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Seq ID NO: 102 Protein sequence:  
 Protein Accession #: NP\_056322.2

1 11 21 31 41 51  
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45 ACCACGCTTC GAGAGCAAGT GGAACCCACC CCTGAGGATG AGGATGATGA CATCGAAGCT 300  
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 CACTGAACCC CATTGCCCTT ACCCTCCTT CTAACCTTAT TGTCTATTCT TCTTCACTCT 6180  
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 AGTGGTTAAG TGC

Seq ID NO: 106 Protein sequence:  
 Protein Accession #: NP\_055883.1

1 11 21 31 41 51  
 MTERRRDELSEENNLREKV MKQSENNNL QSQVQKLTEE NTLREQVEP TPEDEDDIE 60  
 LRGAATAAAP PPIIEECPE DLPEKFDGNP DMLAPFMAQC QIFMEKSTRD FSVDRVRCF 120  
 VTSMMTGRAA RWASAKLERS HYLHNYPAF MMEMKHVFD PORREVAKRK IRLRQMGMS 180  
 VIDYSNAFQM IAQDLWNEP ALIDQYHEGL SDHIQBELSH LEVAKLSAL IGQCIHERR 240

LARAAAARKP RSPPRALVLP HIAASHQVDP TEPVGGARMR LTQBEKERRR KLNLCLYCGT 300  
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Seq ID NO: 107 DNA sequence  
Nucleic Acid Accession #: NM\_003679.1  
Coding sequence: 47-1507 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
10 GGCACGAGCA GAAAGCAACAA TAATTGTGAA AAATACTTCA GCAGTTATGG ACTCATCTGT 60  
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CTTTCTTGCA AAGAGGAATT TCCAGATTGA TGTATATGAA GCTAGGGAAG ATACTCGAGT 180  
GGCTACCTTC ACACGTGGAA GAAGCATTA CTTAGCCCTT TCTCATAGAG GACGACAAGC 240  
CTTGAAAGCT TTGGCCTGG AAGATCAGAT TGTATCCCA GGTATCCCA TGAGAGCAAG 300  
15 AATGATCCAC TCTCTTCAG GAAAAAGTC TGCAATTCCC TATGGGACAA AGTCTCAGTA 360  
TATTCTTCT GTAAGCAGAG AAAATCTAAA CAAGGATCTA TTGACTGCTG CTGAGAAAATA 420  
CCCCAATGG AAAATGCACT TTAACCACAG GCTGTGAAA TGTAAATCCAG AGGAAGGAAT 480  
GATCACAGTG CTTGGATCTG ACAAAGTTC CAAAGATGTC ACTTGTGACC TCATTGTAGG 540  
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20 CAGTCAGCAG TACATTCTCT ATGGGTACAT GGAGTTGACT ATTCCACCTA AGAACGGAGA 660  
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ACTTCTTAAC ATGAACAAAT CATTACATG TACTTTGTTT ATGCCCTTTG AAGAGTTTGA 780  
AAAACTTCTA ACCAGTAATG ATGTGGTAGA TTTCTCCAG AAATACCTTC CGGATGCCAT 840  
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25 GATATCTGTA AAGTGCTCTT CATTACAT TAAATCTCAC TGTGTACTGC TGGGAGATGC 960  
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GGTATTTGAT GAGTTAATGG ATAAATTCAG TAACGACCTT AGTTTGTGTC TTCTGTGTT 1080  
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AGAGATGCGA GCACATGTCA ACTCAAGCTG GTTCATTTT CAGAAGAAC TGGAGAGATT 1200  
30 TCTTCATGCG ATTATGCCAT CGACCTTTAT CCTCTCTAT ACAATGGTCA CTTTTCCAG 1260  
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GTCACCACGA TCTTCTCTCT GCTTGAGAAG ACCATGGAAC TGGATAGCTC ACTTCCGGAA 1440  
TACAACATGT TCCCCGCAA AGGCCGTGGA CTCCTAGAA CAAATTTCCA ATCTCATTAG 1500  
35 CAGGTGATAG AAAGGTTTTG TGGTAGCAA TGCATGATT CTCTGTGACC AAAATTAAGC 1560  
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70 ATTAAGAAAG TTTGTTTTC TTCAACCTCT TCCTGAGGCC CAAGAGCATA TGGGCAATTC 3660  
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75 GAAAGTCACT TTTTCTTTG GCCTGTCCCT ATCTTCTGT GACATCAAA TGGGTCTGAT 3960  
CTGCATTCA CTCCAGCTG CTGGTAGGTC TTAGCAGGC CTCTGGCACC TCAGCAGTCG 4020  
GAGGCACAGA AGCTGCAAAA GGGATCTTCG AAAGTGGGCA GAGAAAAAT AAAGTGGAAAT 4080



ATTAAGTAAA AGTTGGGCAC TAATCTGGAT TAACATTCGA GGAATCAGT TGAGCTGATT 4140  
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Seq ID NO: 108 Protein sequence:

Protein Accession #: NP\_003670.1

1 11 21 31 41 51  
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 RGRQALKAVG LEDQIVSQGI PMRARMHSL SGKKSAPYG TKSQYILSVS RINLNKDLT 120  
 AAEKYPNVKM HFNRHLLKCN PEEGMITVLG SDKVPKDVTC DLVGCDDGAY STVRSHLMKK 180  
 PRFDYSQQYI PHGYMELTIP PKNGDYAMEP NYLHIWPRNT FMMIALPNMN KSFTCTLEMP 240  
 FEEFEKLLTS NDVVDFQKY FPDAPLIGE KLLVQDFLL PAQPMISVKC SSFHFKSHCV 300  
 LLGDAAHAI VPFQGGMNAG FBDCLVDEL MDKFSNDLSL CLPVFSRLRI PDDHAISDLS 360  
 MYNYIEMRAH VNSSWPIFQK NMERFLHAIM PSTFIPLYTM VTFPSRIYHE AVQRWHWQKK 420  
 VINKGLFFLG SLIAISSTYL LIHYMSPRSF LCLRRPWNWI AHFRNTTCFP AKAVDSLEQI 480  
 SNLISR

Seq ID NO: 109 DNA sequence

Nucleic Acid Accession #: NM\_006115.1

Coding sequence: 236-1765 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 CCAACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCTGGCCAT 360  
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 TCTGGGAGTG CTGATGAAAG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540  
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 GGAATTAAGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660  
 TCTGTACTCA TTTCAGAGC CAGAAGCAGC TCAGCCCATG ACAAGAAGC GAAAAGTAGA 720  
 TGGTTTGAAG ACAGAGGCGA AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT 780  
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 TGTGGACTCT TATTTTCTT TTAGAGGCCG CCTGGATCAG TTGCTCAGGC AGTGATGAA 1200  
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Seq ID NO: 110 Protein sequence:

Protein Accession #: NP\_006106.1

1 11 21 31 41 51  
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 5 FDRHRSQTLK AMVQAWPFTC LPLGVLKMGQ HLHLETFKAV LDGLDVLAAQ EVRPRRWKLQ 120  
 VDLRLKNSHQ DFWTVWSGNR ASLYSFEPE AAQPMTKKRK VDGLSTEABQ PFIPVEVLVD 180  
 LFLKEGACDE LFSYLIEKVK RKKNVLRICC KKLKIFAMPM QDIKMILKMV QLDSIEDLEV 240  
 TCTWKLPILA KFSPLYGQMI NLRRLLSHI HASSYISPEK BEQYIAQFTS QFLSLQCLQA 300  
 10 LYVDSLFFLR GRLDQLLRHV MNPLETSLT NCRLESGDVM HLSQSPSVSQ LSVLSLSGVM 360  
 LTDVSPEPLQ ALLERASATL QDLVFDECGI TDDQLLALLP SLSHCSQLTT LSFYGNISIS 420  
 SALQSLQLHL IGLSNLTHVL YVPLESYED IHGTLHLERL AYLHARLREL LCELGRPSMV 480  
 WLSANPCPHC GDRTFYDPEP ILPCPFMPN

15 Seq ID NO: 111 DNA sequence  
 Nucleic Acid Accession #: NM\_003815  
 Coding sequence: 8-2452 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 20 CGCTGCCATG CGGCTGGCGC TGCTCTGGGC CCTGGGGCTC CTGGGCGCGG GCAGCCCTCT 60  
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 35 TGTACCCCTC GAAAACCTCC TCCACTGGCG CAGGGCACAT TTGCTGCCCT GATTGCCCCA 900  
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 40 TGATTGCGCT GGAATAGCT GCCCTGTCC AGGTCCAGCC CCAGCCAAGA CCTGCATCAT 1140  
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 GGAGAAAGCC CTCCTGGATG GAATGGGCG CTGCTCTTC GAACGGCTGC CTAGCCTACC 1260  
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 45 TGCACAGTGT GCATCTGACG GACCCTGTG TCAAAATTGC CAGCTGCCGC CGTCTGGCTG 1440  
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 GTGCATGCAC GGGCGTTGTG CCTCTATGC CCAGCAGTGC CAGTCACTTT GGGGACCTGG 1620  
 AGCCAGCCC GCTGCGCCAC TTGCTCCA GACAGCTAAT ACTCGGGGAA ATGCTTTTGG 1680  
 50 GAGCTGTGGG CGCAACCCCA GTGGCAGTTA TGTGTCTGC ACCCTAGAG ATGCCATTG 1740  
 TGGGCACTC CAGTGCAGCA CAGGTAGGAC CCAGCCTCTG CTGGGCTCCA TCCGGGATCT 1800  
 ACTCTGGGAG ACAATAGATG TGAATGGGAC TGAGCTGAAC TGCACTGTGG TGACCTTGA 1860  
 CCTGGGCACT GATGTGGCCC AGCCCTCTCT GACTCTGCTT GGCACAGCCT GTGGCCCTGG 1920  
 CCTGTGTGT ATAGACCATC GATGCCAGCG TGTGGATCT CTGGGGGCAC AGGAATGTGC 1980  
 55 AAGCAAATGC CATGGACATG GGTCTGTGA CAGCAACAGG CACTGCTACT GTGAGGAGGG 2040  
 CTGGGCAACC CCTGACTGCA CCCTCAGCT CAAAGCAACC AGCTCCCTGA CCACAGGGCT 2100  
 GCTCTCAGC CTCCTGGTCT TATGGTCTT GGTGATGCTT GGTGCCGCT ACTGGTACCG 2160  
 TGCCCGCCTG CACGAGGAC TCTGCCAGCT CAAGGAGACC ACCTGCCAGT ACAGGGCAGC 2220  
 CCAATCTGCT CCCTCTGAAC GGCCAGGACC TCCGAGAGG GCCCTGCTGG CACGAGGCAC 2280  
 60 TAAGTCTCAG GGGCCAGCCA AGCCCCACC CCAAGGAAG CCCTGCTG CCGACCCCA 2340  
 GGGCCGGTGC CCATCGGGT ACCTGCCCG CCCAGGGGCT GGAATCCCG CCCTAGTGGT 2400  
 ACCCTCCAG CAGCGCCAC CGCCTCCGAC AGTGTCTCTG CTCTACCTCT GACCTCTCCG 2460  
 GAGGTCTCCG TGCCCTCCAAG CCGGACTTAG GGCTTCAAGA GCGGGCGGTG CCTCTGGAG 2520  
 TCCCTACCA TGAAGTGAAG CGCCAGAGAC TGGCGGTGTC TTAAGACTCC GGGCACCAGC 2580  
 65 ACGCGCTGTG AAGCAACAT CTGCGGACCT GCGGGCGTAG TTGAGCGGG GCGTTGGGA 2640  
 GGGGCTGGGG GTTGGACGGG ATTGAGGAAG GTCCGCACAG CCTGTCTCTG CTCAGTTGCA 2700  
 ATAAACGTGA CATCTGGGA GCGTTAAAAA AAAAAAAAAA

Seq ID NO: 112 Protein sequence:  
 Protein Accession #: NP\_003806.2

1 11 21 31 41 51  
 70 MRLALLWALG LLGAGSPLPS WPLPNIGGTE EQQAESKAP REPLEPQVLQ DDLPLSLKKV 60  
 LQTSLEPLR IKLELDGDSH ILELLQNREL VPGRTLVVY QPDGTRVSE GHTLENCCYQ 120  
 75 GRVRYAGSW VSICTCSGLR GLVVLTPERS YTLQGGPDL QGPPHSRIQ DLHLPHTCA 180  
 LSWRESVHTQ TPPEHPLQR HRRRDVVT ETKTVELVIV ADHSEAQYR DFQHLNRTL 240  
 EVALLDITFF RPLNVRVALV GLEAWTQRDL VEISPNPAVT LENFLHWRRA HLLPRLPHDS 300

AQLVTGTSFS GPTVGMAIQN SICSPDFSGG VNMDHSTSL GVASSIAHEL GHSLGLDHDH 360  
 PGNSCPGPG APAKTCIMEA STDPLGLNF SNCRRRALEK ALLDGMGSL FERLPSLPPM 420  
 AAFCGNMFBV PGEQDCGFL DDCVDPCDS LTCQLRPGAQ CASDGPCCQN CQLRPSGWQC 480  
 RPTRGDCDLP EFCPGDSSQC PPDVSLGDGE PCAGGQAVCM HGRCASYAQ CQSLWGPQAQ 540  
 PAAPLCLQTA NTRGNAPGSC GRNPSGSYVS CTPRDAICGQ LQCQTGRTP LLGSIRDLLW 600  
 ETIDVNGTEL NCSWVHLDLG SDVAQPLLT PGTACGPGLV CIDHRCQRVD LLGAQECRSK 660  
 CHGHGVCDN RHCYCEGWA PPDCTTQLKA TSSLTTGLLL SLLVLLVLM LGAGYWYRAR 720  
 LHQRLCQLKG PTCQYRAAQ GPSPRPQPQ RALLARGTKS QGPAKPPPPR KPLPADPQGR 780  
 CPSGDLPGPG AGIPLVVPF RPAPPPPTVS SLYL

Seq ID NO: 113 DNA sequence

Nucleic Acid Accession #:

NM\_002416

Coding sequence: 40-417 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATCCAATACA GGAGTGACTT GGAATCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTT 60  
 TTCCTCTTGG GCATCATCTT GCTGGTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120  
 AAGGGTCGCT GTTCTGTCAT CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA 180  
 GACCTTAAAC AATTGCCCC AAGCCCTCC TCGGAGAAAA TTGAATCAT TGCTACACTG 240  
 AAGAAATGGAG TTCAAACATG TCTAAACCCA GATTCAGCAG ATGTGAAGGA ACTGATTAAA 300  
 AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360  
 AAGAAAGTTC TGAAGATTGG AAAATCTCAA CGTTCTCGTC AAAAGAAGAC TACATAAGAG 420  
 ACCACTTCAC CAATAAGTAT TCTGTGTAA AAATGTTCTA TTTAATTAT ACCGCTATCA 480  
 TTCCAAAGGA GGATGGCATA TAATCAAAAG GCTTATTAAT TTGACTAGAA AATTAAAAAC 540  
 ATTACTCTGA AATTGTAAT AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACCTTAAGAA 600  
 TTGTTAAAGG CTATGATTGT CTTTGTCTT CTACCACCCA CCAGTTGAAT TTCATCATGC 660  
 TTAAGGCCAT GATTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATCCCA 720  
 CTCACAACAG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCAGAGAG 780  
 TATCTGAGGC ACATGTACAG AAGTCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT 840  
 TGAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900  
 CTACAGGCCT CACACACAAT GTGCTGAGA GATTCATGCT GATTGTTATT GGGTATCACC 960  
 ACTGGAGATC ACCAGTGTGT GGCTTTCAGA GCCTCCTTTC TGGCTTGGGA AGCCATGTGA 1020  
 TTCCATCTTG CCGCTCAGG CTGACCACTT TATTCTTTT TGTTCCTT TGCTTCATTC 1080  
 AAGTCAGCTC TCTCCATCC TACCACAATG CAGTGCCTT CTCTCTCCA GTGCACCTGT 1140  
 CATATGCTCT GATTATCTG AGTCAACTCC TTTCTCATCT TGTCCTCAAC ACCCCACAGA 1200  
 AGTGTCTTCT TCTCCCAAT CATCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260  
 AAATAAACCT TTTTGACAC ACAATTATC TAAAACTCC TGTTCACTT GGTTCAGTAC 1320  
 CACATGGGTG AACACTCAAT GTTAACTAA TTCTTGGGTG TTTATCTAT CTCTCAACC 1380  
 AGATTGTAG CTCTTGTAGG GCAAGAGCCA CAGTATATT CCCTGTTTCT TCCACAGTGC 1440  
 CTAATAATAC TGTGGAAGTA GGTTTAATA ATTTTAAAT TGATGTTGT ATGGGACGGA 1500  
 TGGCAACCAAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560  
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACACAGG GACCAGGGAT 1620  
 GATGCAACAT CCTTGTCTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680  
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740  
 AAAATCATAT AATCTTACAA TGAAGAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800  
 CCAACCATAC AAAAATTCCT TTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860  
 TCTAAGATCT AACAAGATAG CCACCGAGAT CCTATCGAA ACTCATTTTA GGCAAAATATG 1920  
 AGTTTATATG TCGTTTACT TGTTCAGAG TTTGTAATGT GATTATCAAT TACCACACCA 1980  
 TCTCCCATGA AGAAAGGGA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040  
 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAACCC TCCTTCCAGG 2100  
 GGAGGTTTCA GTAATTGTTG AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160  
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATT AGAGTGTCTG CCGGTGGAGA 2220  
 TCCACCCGGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280  
 AAAATCTTAA GTGTTTCATA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340  
 GTAGACAGTA TATAACTAAC AACCAAGAC FACATATTGT CACTGACACA CACGTTATAA 2400  
 TCATTATCA TATATATACA TACATGCATA CACTCTCAA GCAAAATATT TTTCACTTCA 2460  
 AAACAGTATT GACTGTGATA CCTGTGAAT TGAATATTT TCTTTGTAA AATAGAATGG 2520  
 TATCAATAAAA TAGACCATTA ATCAG

Seq ID NO: 114 Protein sequence:

Protein Accession #:

NP\_002407

1 11 21 31 41 51  
 MKKSGVLFLL GILLVLVIG QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSFSCEK 60  
 IEHATLKNV QYCLNPDSA DVKELIKKWE KQVSQKKKKQ NGKKHQKKV LKVRKSQRSR 120  
 QKKTT

Seq ID NO: 115 DNA sequence

Nucleic Acid Accession #:

NM\_003238.1

Coding sequence: 182-1426 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CAAGCAGGAT ACGTTTCT GTTGGGCATT GACTAGATTG TTGCAAAAG TTTCGCATCA 60  
 AAAACAAACA ACAACAACA AAAACCAAC AACTCTCTT GATCTATACT TTGAGAATTG 120

TTGATTTCCTT TTTTITTAAT CTGACTTTTA AAAACAACCTT TTTTTCAC TTTTAAAA 180  
 AATGCACTAC TGTGTGCTGA GCGCTTTCT GATCCTGCAT CTGGTCACGG TCGCGCTCAG 240  
 CCTGTCTACC TGCAGCACAC TCGATATGGA CCAGTTCATG CGCAAGAGGA TCGAGGCGAT 300  
 CCGCGGGCAG ATCCTGAGCA AGCTGAAGCT CACCACTCCC CCAGAAGACT ATCCTGAGCC 360  
 5 CGAGGAAGTC CCCCCGAGG TGATTTCAT CTACAACAGC ACCAGGGAAT TGCTCCAGGA 420  
 GAAGGCGAGC CGGAGGGGCG CCGCTGCGA GCGCGAGAGG AGCGACGAAG AGTACTACGC 480  
 CAAGGAGGTT TACAAAATAG ACATGCCGCC CTTCCTCCCC TCCGAAAAATG CCATCCCCGCC 540  
 CACITTTCTAC AGACCCTACT TCAGAAATGT TCGATTGAC GTCTCAGCAA TGGAGAAGAA 600  
 10 TGCTTCCAAT TTGGTGAAG CAGAGTTCAG AGTCTTTCGT TTGCAGAAC CCAGAGCCAG 660  
 AGTGCCTGAA CAACGGATTG AGCTATATCA GATTCTCAAG TCCAAAGATT TAACATCTCC 720  
 AACCAGGCGC TACATCGACA GCAAAAGTTG TGAACAAGA GCAGAAGGCG AATGGCTCTC 780  
 CTTCGATGTA ACTGATGCTG TTCATGAATG GCITCACCAT AAAGACAGGA ACCTGGGATT 840  
 TAAAAAAGC TTACACTGTC CCTGCTGCAC TTTGTACCA TCTAATAAT ACATCATCCC 900  
 15 AATAAAAGT GAAGAAGTAG AAGCAAGATT TGCAGGTATT GATGGCACCT CCACATATAC 960  
 CAGTGGTGAT CAGAAAACTA TAAAGTCCAC TAGGAAAAAA AACAGTGGGA AGACCCACA 1020  
 TCTCTGCTA ATGTATTGCT CCTCTACAG ACTTGAGTCA CAACAGACCA ACCGGCGGAA 1080  
 GAAGCGTGCT TTGGATGCGG CCTATTGCTT TAGAAATGTG CAGGATAATT GCTGCTTACG 1140  
 TCCACTTTAC ATTGATTTC AAGGGGATCT AGGGTGGAAA TGGATACAGC AACCCAAAGG 1200  
 20 GTACAATGCC AACTTCTGTG CTGGAGCATG CCCGTATTTA TGGAGTTCAG AACTCAGCA 1260  
 CAGCAGGGTC CTGAGCTTAT ATAATACCAT AATCCAGAA GCATCTGCTT CTCCTTGTG 1320  
 CGTGTCCCAA GATTAGAAC CTCTAACCAT TCTCTACTAC ATTGGCAAAA CACCCAAGAT 1380  
 TGAACAGCTT TCTAATATGA TTGTAAAGTC TTGCAAAATG AGCTAAAAAT CTGGGAAAAG 1440  
 TGGCAAGACC AAAATGACAA TGATGATGAT AATGATGATG ACGACGACAA CGATGATGCT 1500  
 25 TGTAACAAGA AACATAAGA GAGCCITGGT TCATCAGTGT TAAAAAATTT TTGAAAAGGC 1560  
 GGTACTAGTT CAGACACTTT GGAAGTTTGT GTTCTGTTTG TAAAACTGG CATCTGACAC 1620  
 AAAAAAGATT GAAGGCCITA TTCTACATT CACCTACTTT GTAAGTGAGA GAGACAAGAA 1680  
 GCAAAATTTT TAAA

Seq ID NO: 116 Protein sequence:  
 Protein Accession #: NP\_003229.1

1 11 21 31 41 51  
 } } } } }  
 35 MHYCVLSAFL ILHLVTVALS LSTCSTLMD QFMRKRIBAI RGQILSKLKL TSPEDYPEP 60  
 EEVPEVISI YNSRDLLE KASRRAAACE RERSDEEYVA KEVYKIDMPP FFPSENAIPP 120  
 TFYRPFYFRV RFDVSAMEKN ASNLVKAERF VRLQNPKE VPEQRIELYQ ILKSKDLTSP 180  
 TQRYIDSKVV KTRAGEBWLW PDVTDVHEW LHHKDRNLGF KISLHCPCTT FVPSNNYIP 240  
 NKSEBLEARF AGIDGTSTYT SGDQKTIKST RKKNSGKTPH LLLMLPSYR LESQQTNRK 300  
 40 KRALDAAYCF RNVQDNCCLR PLYIDFKRDL GWKWIHEPKG YNANFCAGAC PYLWSSDTQH 360  
 SRVLSLYNTI NPEASAPCC VSQDLEPLTI LYYIGKTPKI BQLSNMIVKS CKCS

Seq ID NO: 117 DNA sequence  
 Nucleic Acid Accession #: NM\_000095.1  
 Coding sequence: 26-2299 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 } } } } }  
 45 CAGCACCCAG CTCCCGGCCA CCGGCAATGGT CCGGACACC GCCTGCGTTC TTCTGCTCAC 60  
 CCTGGCTGCC CTGCGCGCGT CCGGACAGGG CCAGAGCCCC TTGGGCTCAG ACCTGGGCCC 120  
 50 GCAGATGCTT CCGGAAGTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180  
 GCGGCAGCAG GTCAGGGAGA TCACGTTTCT GAAAAACACG GTGATGGAGT GTGACGCGTG 240  
 CCGGATGCAAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCTTGC TCCACTGCGC 300  
 GCGCGGCTTC TGCTTCCCG CGTGCGCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG 360  
 55 CCCCTGCCCC GCGGGCTTCA CCGGCAACCG CTGCACTGC ACCGACGTCA ACGAGTGCAA 420  
 CGCCCAACCC TGCTTCCCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480  
 GGCTTGCCCG CCGGGGTACA GCGGCCAC CCACCAGGGC GTGGGGCTGG CTTTCGCCAA 540  
 GGCCAACAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGGT 600  
 CCCCACCTCC GTGTGCATCA ACACCGGGG CTCTTCCAG TGCGGCCGTG GCCAGCCCGG 660  
 60 CTTCGTGGG GACCAAGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGGACGG 720  
 CTCGCGGAGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780  
 GTGCGTGTGT CCGGTGGCT GGGCGGCA CCGGATCCTC TGTGGTGGG AACTGACCT 840  
 AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCCG CAGTGCCGTA AGGACAACCTG 900  
 CGTGACTGTG CCAACTCAG GGCAGGAGGA TGTGGACCGG GATGGCATCG GAGACGCTG 960  
 65 CGATCCGGAT GCCAGCGGG ACGGGGTCCC CAATGAAAAG GACAACCTGC CGCTGGTGCG 1020  
 GAACCCAGAT CCGGCAACA CCGGAGGGA CAAGTGGGGG GATGCGTGCG ACAACTGCCG 1080  
 GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAGGAG GCGCGGGGCG ATGCGTGCGA 1140  
 CGACGACATC GACGGGACC GGATCCGCAA CCAGGCGGAC AACTGCCCTA GGTACCCAA 1200  
 CTCAGACACC AAGGACAGTG ATGGCGATGG TATAGGGGAT CCGTGTGACA ACTGTCCCA 1260  
 GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320  
 70 CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACCTGC CCACGGTGCC 1380  
 TAACAGTGCC CAGGAGGACT CAGACACGA TGGCCAGGGT GATGCGTGCG ACGACGACGA 1440  
 CGACAATGAC GGAGTCCCTG ACAGTCCGGA CAACTGCCCG CTGGTGCTTA ACCCGGCCA 1500  
 GGAGGACGCG GACAGGGAGC GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560  
 GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620  
 75 GGCCTTCCAG ACAGTCGTG TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680  
 GGTGCTAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740  
 GGGTTACACT GCCTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC 1800

GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860  
 CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCTTCCGTG CTGTGGCCGA 1920  
 GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980  
 CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040  
 5 AAACGTGGGT TGGAAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGGCCCAAGT 2100  
 GGGCTACATC AGGGTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160  
 CTTGGACACA ACCATGCGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCC AGGAGAACAT 2220  
 CATCTGGGCC AACCTGCGTT ACCGTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280  
 10 TCAGCTGCGG CAAGCCTAGG GACCAGGGT AGGACCCGCC GGATGACAGC CACCCTCACC 2340  
 GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAAGTGAG 2400  
 AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG

Seq ID NO: 118 Protein sequence:  
 Protein Accession #: NP\_00086.1

1 11 21 31 41 51  
 MYPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDV RD WLRQQVREIT 60  
 20 FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120  
 NGSHTDVNE CNAHPCFPRV RCINTSPGFR CEACPPQYSG PTHQGVQLAF AKANKQVCTD 180  
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240  
 ADCVLERDGS RSCVCRV GWA GNGILCGRDT DLDGFPDEKL RCPBPQCRKD NCVTVPNSGQ 300  
 EDVDRDGIGD ACDPDADG DG VPNEKDNCL VRNPQQRNTD EDKWGDACDN CRSQKNDDQK 360  
 DTDQDGRGDA CDDIDGDR I RNQADNCP RV PNSDQKDS DG DGIGDACDNC PQKSNPDQAD 420  
 25 VDHFVGDAC DSDQDQDGD G HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPDS 480  
 RDNCRLVNP GQEDADR DG V GDVCCDDFDA DKVVVDKIDV C PENA EVTLTD FRAFQTVVLD 540  
 PEGDAQIDFN WVVNLNQG REI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600  
 FGYQDSSSFY VVMWKQMEQT YWQANPFR AV AEPGIQLKAV KSSTGPGBEQL RNALWHTGDT 660  
 30 ESQVRLWKID PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPBLVADSN VVLDTTMRGG 720  
 RLGVFCSQE NIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 119 DNA sequence  
 Nucleic Acid Accession #: NM\_014211  
 Coding sequence: 157-1479 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGGACAGGCG TGAGGATGAG GAGAACCCTG GGGACCCAGA AGACCGTGCC TTGCCCGGAA 60  
 40 GTCTGCGCTG TAGGCTGAAA GGACTTGCCC TAACAGAGCC TCAACAACCTA CCTGGTGATT 120  
 CCTACTTCAG CCCCTTGGTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACCTGGCC 180  
 TTCGTGTGTC TGAGTCTCTT CACTGAGAGG ATGTGCATCC AGGGGAGTCA GTTCAACGTC 240  
 GAGGTGCGCA GAAGTGACAA GCTTCCCTG CCTGGCTTTG AGAACCTCAC AGCAGGATAT 300  
 AACAAATTTT TCAGGCCCAA TTTTGGTGGG GAACCCGTAC AGATAGCGCT GACTCTGGAC 360  
 45 ATTGCAAGTA TCTCTAGCAT TTAGAGAGT AACATGGACT ACACAGCCAC CATATACCTC 420  
 CGACAGCGCT GGATGGACCA GCGGCTGGTG TTTGAAGGCA ACAAGAGCTT CACTCTGGAT 480  
 GCGCGCTCGT TGGAGTTCCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540  
 TTCTCTCATG AGTTCATGT GGGAAACAGG CTCATCCGCC TCTCTCCAA TGGCACGGTC 600  
 CTGTATGCCC TCAGAATCAC GACAACCTGT GCATGTAACA TGGATCTGTC TAAATACCCC 660  
 ATGGACACAC AGACATGCAA GTTGCAGCTG GAAAGCTGGG GCTATGATGG AAATGATGTG 720  
 50 GAGTTCACCT GGCTGAGAGG GAACGACTCT GTGCGTGGAC TGAACACCT GCGGCTTGCT 780  
 CAGTACACCA TAGAGCGGTA TTTACCTTA GTCACCAGAT CGCAGCAGGA GACAGGAAAT 840  
 TACACTAGAT TGGTCTTACA GTTTGAGCTT CGGAGGAATG TTCTGTATTT CATTTTGGAA 900  
 ACCTACGTTT CTTCACCTT CTGGTGGTG TTGTCCTGGG TTTCATTTTG GATCTCTCTC 960  
 55 GATTACGTCC CTGCAAGAAC CTGCATTGGA GTGACGACCG TGTATCAAT GACCACACTG 1020  
 ATGATCGGGT CCCGCACTTC TCTTCCCAAC ACCAAGTCTT TCATCAAGGC CATCGATGTG 1080  
 TACCTGGGGA TCTGCTTAG CTTTGTGTTT GGGGCTTGC TAGAATATGC AGTTGCTCAC 1140  
 TACAGTTCTT TACAGCAGAT GGCAGCCAAA GATAGGGGGA CAACAAAGGA AGTAGAAGAA 1200  
 GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TAAACGGGA GATCAGCTTT 1260  
 60 GCCAGCATTT AAATTTCCAG CGACAACGTT GACTACAGTG ACTTGACAAT GAAAACCAAGC 1320  
 GACAAGTTCA AGTTGTCTT CCGAGAAAAG ATGGGCAGGA TGTGTGATTA TTTCACAATT 1380  
 CAAAACCCCA GTAATGTTGA TCACTATTCC AAACCTACTG TTCTTTGAT TTTTATGCTA 1440  
 GCCAATGTAT TTTACTGGGC ATACTACATG TATTTTIGAG TCAATGTTAA ATTTCTTGCA 1500  
 TGCCATAGGT CTTCACAGG ACAAGATAAT GATGTAAATG GTATTTTAGG CCAAGTGTGC 1560  
 65 ACCCACATCC AATGGTGCTA CAAGTGACTG AAATAATATT TGAGTCTTTC TGCTCAAAGA 1620  
 ATGAAGCTCC AACCATGTT CTAAGCTGTG TAGAAGTCTT AGCATTATAG GATCTTGTA 1680  
 TAGAAACATC AGTCCATTCC TCTTCATCT TAATCAAGGA CATTCCCATG GAGCCCAAGA 1740  
 TTACAAATGT ACTCAGGGCT GTTTAATCGG TGGCTCCCTG GTTTCATTTT ACCTCATATA 1800  
 AAGAAATGGA AGGAGACCAT TGGTAACCC TCAAGTGTCA GAAGTTGTTT CTAAGGTAAC 1860  
 70 TATACATGTT TTTTACTAAA TCTTCGAGT GCTTATAAAA TACATTGTTG CCTATTIAGG 1920  
 GAGTAACATT TTCTAGTTTT TGTITCTGTT TAAATGAAA TATGGGCTTA TGTCAAATTA 1980  
 TTGGAAGTCA ATGCACTAAT TGGTAACCA GATGAGTTT TAAATAATGA ATATTATTTA 2040  
 ATACCACAAC AGAATATATC CCAATTTCCA ATAAAGTCTA TCATTGAAAA TTCAAATATA 2100  
 AGTGAAGAAA AAATTAGTAG ATCAACAATC TAAACAATC CCTCGGTTCT AAGATACAAT 2160  
 75 GGATTTCCCA TACTGGAAGG ACTCTGAGGC TTTATTTCCC CACTATGCAT ATCTTATCAT 2220  
 TTTATTATTA TACACACATC CATCTAAAC TATACTAAAG CCTTTTCCC ATGCATGGAT 2280  
 GGAATGGGAA GATTTTTTTC TAACTTGTTT TAGAAGTCTT AATATGGGCT GTTGCCATGA 2340  
 AGGCTTGCA G AATTGAGTCC ATTTCTAGC TGCCTTTATT CACATAGTGA TGGGGTACTA 2400

AAAGTACTGG GTTGACTCAG AGAGTCGCTG TCATTCTGTC ATTGCTGCTA CTCTAACACT 2460  
 GAGCAACACT CTCCCAGTGG CAGATCCCCT GTATCATTCG AAGAGGAGCA TTCATCCCCT 2520  
 TGCTCTAATG ATCAGGAATG ATGCTTATTA GAAACAAAC TGCTTGACCC AGGAACAAGT 2580  
 GGCTTAGCTT AAGTAAACTT GGCCTTGCTC AGATCCCCTG TCCTTCCAGC TGGTCTGCTC 2640  
 5 TGAGTGGCTT ATCCCGCATG AGCAGGAGCG TGCTGGCCCT GAGTACTGAA CTTTCTGAGT 2700  
 AACAAATGAGA CACGTTACAG AACCTATGTT CAGGTTGCCG GTGAGCTGCC CTCTCCAAAT 2760  
 CCAGCCAGAG ATGCACATTC CTCGGCCAGT CTCAGCCAAC AGTACCAAAA GTGATTTTGG 2820  
 AGTGTGCCAG GGTAAAGGCT TCAGTTCAG CCTCAGTTAT TTAGACAAT CTCGCCATCT 2880  
 TTAATTTCTT AGCTTCCTGT TCTAATAAAT GCACGGCTTT ACCTTCCCTG TCAGAAATAA 2940  
 10 ACCAAGGCTC TAAAAGATGA TTCCCTTCT GTAACCTCC AGAGCCACAG GTTCTCATTC 3000  
 CTTTTCCCAT TATACITCTC ACAATTCAGT TTCTATGAGT TTGATCACCT GATTTTITTA 3060  
 ACAAATATTT TCTAACGGGA ATGGGTGGGA GTGCTGGTGA AAAGAGATGA AATGTGGTGG 3120  
 TATGAGCCAA TCATATTTGT GATTTTITTA AAAAAGTTA AAAGGAAATA TCTGTTCTGA 3180  
 15 AACCCCATIT AAGCATTTGT TTTATATAAA AACAATGATA AAGATGTGAA CTGTGAAATA 3240  
 AATATACCAT ATTAGCTACC CACC

Seq ID NO: 120 Protein sequence:  
 Protein Accession #: NP\_055026.1

1 11 21 31 41 51  
 | | | | |  
 MNYSLHLAFV CLSLFTEPMC IQGSGFNVEV GRSDKLSLPG FENLTAGYNK FLRPNFGGEP 60  
 VQIALTLIDIA SSSISESNM DYTATVLRQ RWMDQRLVE GNKSFTLDAR LVEFLWVDPD 120  
 YIVESKKSFL HEVTVGNRLI RLFSNGTVLY ALRITTVAC NMDLSKYPMD TQTCKLQLES 180  
 25 WGYDGNDFEF TWLRGNDVSR GLBHLRLAQY TIERYFTLVT RSQETGNYT RLVQLQELRR 240  
 NVLYFILETY VPSTFLVLS WVSFWISLDS VPARTCIGVT TVLSMTTLM I GSRTSLPNTN 300  
 CFKADIVYL GICFSFVGA LLEYAVAHYS SLQMAAKDR GTTKEVEEVS ITNINSSIS 360  
 SFKRKISFAS IEISSDNVDY SDLTMTKTSK FKFVFRKMG RIVDYFTIQN PSNVDHYSKL 420  
 LPLIFMLAN VFYWAYYYMYF

Seq ID NO: 121 DNA sequence  
 Nucleic Acid Accession #: NM\_001854  
 Coding sequence: 163-5582 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 50 GAACAAGGAT TTGGATGAA GAAGTTTTG AGGGGGACAT TCAGCAGTTT TTGATCACAG 840  
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 55 GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080  
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 60 AAGAATATGA AGATAAACA ACAAGCCCC CTAAATGAAGA ATTTGGTCCA GGTGTACCA 1380  
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 10 ACCCTGGGCA ACGTGGGGAG ACTGGATTTC AAGGCAAGAC CGGCCCTCCT GGGCCAGGGG 3060  
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 60 TGTGTTAAT AAATGTGTAAT TATTTGTGT ACAGTTCIAT ACTGTTATCT GTGTCCATTT 6000  
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Seq ID NO: 122 Protein sequence:  
 Protein Accession #: NP\_001845

1 11 21 31 41 51  
 70 MEPWSSRWKT KRWLWDFVT TLALTLFQA REVGAAPVD VLKALDFHNS PEGISKTTGF 60  
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 EHGIIQIGVE VGRSPVFLFE DHTGKPAFED YPLFRVFNIA DGKWHRVAS VEKKTVTMIV 180  
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 75 PDCDSSAPKA AQAQEPQIDE YAPEDIIEYD YBYGEAEYKE AESVTEGPTV TEETIAQTEA 300  
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 PVCFLG

Seq ID NO: 123 DNA sequence  
 Nucleic Acid Accession #: NM\_015886  
 Coding sequence: 485-1261 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 35 ATGGTTTACA TTCATTTAG GGTAGTGGT CATGCTGTT ATTTTCTCT GCTATACAAA 240  
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 40 CAAATGATA GCAATCTCT CCGTCAGCAG TGCACCTCT TCTCCCTTC TCTGTGAAGC 540  
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 55 AGTATTCCT TGTATAAAT AGTGTGTC TAGCATGTT GTTTAATCT TGGGAATTC

Seq ID NO: 124 Protein sequence:  
 Protein Accession #: NP\_056970.1

1 11 21 31 41 51  
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 60 MIAISAVSSA LLFSLLEAS TVVLLNSTDS SPTNNFTDI EAALKAQLDS ADIPKARRKR 60  
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 65 SNRIGCAIHA CQNMNVWGSV WRRAYLVCN YAPKGNWIGE APYKVGVPSC SCPPSYGGSC 240  
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Seq ID NO: 125 DNA sequence  
 Nucleic Acid Accession #: NM\_001793  
 Coding sequence: 54-2543 (underlined sequences correspond to start and stop codons)

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 CGGAGCAGGA GCGCGGCGC GCGCTGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240



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Seq ID NO: 126 Protein sequence:  
 Protein Accession #: NP\_001784

1 11 21 31 41 51  
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 KGFPPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREBIK 180  
 YELFGHAVSE NGASVEDPMN ISIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAITYN GVVAYSISHP EPKDPHDLMF TIHRSTGTS VISSGLDREK VPEYTLTIQA 300  
 TDMDDGDSST TAVAVVEILD ANDNAPMFDQ QKYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYLMG GDDGDHFTTT THPESNQGL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPFSKYVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMPD DSGQVTA VGT LDREDEQFVR NNIYEVMLA MDNGSPPTG TGTLLTLID 540  
 VNDHGPVPEP RQITCNQSP VRHVLNITDK DLSFHTSPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KDQTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPG WKGGFILPVL 660  
 GAVLALLFL LVLALLVRKK RKKEPLL EDDTRDNV FY YGHEGGGEEQ QDYDITQLHR 720  
 GLEARFEVL RNDVAPTIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEAGSGSDA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 127 DNA sequence  
 Nucleic Acid Accession #: NM\_003256.1  
 Coding sequence: 60-734 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCTGCTGGGG CCGTCCAGTC CCCAGACCT CACAGGCTCA GTCGCGGATC TGCAGTGTC 60

TGCCTGGGAG CCCTCGGCC GCGCCAAGCT GGGTGCCTTT GCTGCGGCTG CTGGCGTTGC 120  
 TGCGGCCCCC GGGGCTGGGT GAGGCATGCA GCTGCGCCCC GGCGCACCCCT CAGCAGCACA 180  
 TCTGCCACTC GGCACCTTGT ATTGCGGCCA AAATCTCCAG TGAGAAGGTA GTTCCGGCCA 240  
 GTGCAGACCC TGCTGACACT GAAAAAATGC TCCGGTATGA AATCAAACAG ATAAAGATGT 300  
 TCAAAGGGTT TGAGAAAGTC AAGGATGTT AGTATATCTA TACGCCTTTT GACTCTTCCC 360  
 TCTGTGGTGT GAAACTAGAA GCCAACAGCC AGAAGCAGTA TCTCTTGACT GGTCAAGTCC 420  
 TCAGTGATGG AAAAGTCTTC ATCCATCTGT GCAACTACAT CGAGCCCTGG GAGGACCTGT 480  
 CCTTGGTGCA GAGGGAAGT CTGAATCATC ACTACCATCT GAACTGTGGC TGCCAAATCA 540  
 CCACCTGCTA CACAGTACCC TGTACCATCT CGGCCCTTAA CGAGTGCCTC TGGACAGACT 600  
 GGCTGTTGGA ACGAAAGCTC TATGGTTACC AGGCTCAGCA TTATGTCTGT ATGAAGCATG 660  
 TTGACGGCAC CTGCAGCTGG TACCGGGGCC ACCTGCCTCT CAGGAAGGAG TTTGTTGACA 720  
 TCGTTCAGCC CTAGTAGGGA CCAAGTGACCA TCACATCCCT TCAAGAGTCC TGAAGATCAA 780  
 GCCAGTCTC CTCCCTGCA GAGCTTTGGC CATTACCACC TGACCTCTTG CTGCCAGCTA 840  
 ATAAGAAGTG CCAAGTGGAC AGTCTGGCCA CTGTCAAGGC AGGGAAGGGG CCATGACTTT 900  
 TCTGCCCTGC CCTCAGCTGT TTGCCCTGCC TCCAAACCC CATTAGTCTA GCCTTGTAGC 960  
 TGTTACTGCA AGTGTTCCTT CTGGCTTAGT CTGTTTCTA AAGCCAGGAC TATCCCTTT 1020  
 CCTCCCCAGG AATATGTGTT TICTTTGTC TTAATCGATC TGGTAGGGGA GAAATGGCGA 1080  
 ATGTCATACA CATAGATGG TATATCCTTG CGATGTACAG AATCAGAAGG TGGTTTGACA 1140  
 GCATCATAAA CAGGCTGACT GGCAGGAATG AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 128 Protein sequence:  
 Protein Accession #: NP\_003247.1

1 11 21 31 41 51  
 MPGPSRPAPS WVLLRLRLAL IRPPLGEAC SCAPAHPPQH ICHSALVIRA KISSEKVVPA 60  
 SADPADTEKM LRYEIKQIKM FKGFVKVDV QYIYTFDSS LGGVKLEANS QKQYLLTGQV 120  
 LSDGKVFHIL CNYIEPWEDL SLVQRESLNI HYHLNCGCQI TICYTVPCIT SAPNECLWTD 180  
 WLLERKLYGY QAQHYVCMKH VDGTCWSYRG HPLRKEFVD IVQP

Seq ID NO: 129 DNA sequence  
 Nucleic Acid Accession #: NM\_007207.2  
 Coding sequence: 143-1591 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCACGCGTCC GCAATGAAGC CGAGTGAATG GGGGCTGAAT GTGCGAGTCC ATAGCTGAAG 60  
 AGGAGCGCCA GATGGTGGAG GAATACACTT ATTTATGAAA CTGTCTTGAG TTCTTCTTGA 120  
 ATTGCCAGTT TTAGCCTTCC TATGCTCTCC GTCTCCTTTA GACGACAGGG TAGTAGTGGC 180  
 ACTATCTAGG CCGGTCGGAC CTGAGGATCT CAACCTTTGT TTAGACTCTA GTTACCTTGG 240  
 CTCTGCCAAC CCAGGCAGTA ACAGCCACCC TCCTGTCATC GCCACCACCG TTGTGTCCCT 300  
 CAAGGCTGGG AATCTGACGT ATATGCCCTC ATCCAGCGGC TCTGCCCGCT CGCTGAATTG 360  
 TGGATGCAGC AGTGCCAGCT GCTGCACTGT GGCAACCTAC GACAAGGACA ATCAGGCCCA 420  
 AACCCAAGCC ATTGCCGCTG GCACCACCAC CACTGCCATC GGAACCTCTA CCACCTGCCC 480  
 TGCTAACAGC ATGGTCAACA ATAATGAGAA TACAGGCTCT CTAAGTCCAT CAAGTGGGGT 540  
 GGGCAGCCCT GTGTCAAGGA CCCCCAAGCA GCTAGCCAGC ATCAAATAA TCTACCCCAA 600  
 TGACTTGGCA AAGAAGATGA CCAATGTCAG CAAGAGTCAC CTGCCGAGTC AGGGCCCTGT 660  
 CATCATGAC TGCAAGCCCT TCATGGAGTA CAACAAGAGT CACATCCAAG GAGCTGTCCA 720  
 CATTAAGTGT GCGCTAAGGA TCAGCCGCGG GAGACTGCAG CAGGGCAAGA TCACTGTCTT 780  
 AGACTTGATT TCTGTAGGG AAGGCAAGGA CTCTTCAAG AGGATCTTTT CCAAGAAAT 840  
 TATAGTTTAT GATGAGAATA CCAATGAACC AAGCCGAGTG ATGCCCTCCC AGCCACTTCA 900  
 CATAGTCTCT GAGTCCCTGA AGAGAGAAGG CAAAGAACCT CTGGTGTGGA AAGGTGGACT 960  
 TAGTAGTTT AAGCAGAACC ATGAAAACCT CTGTGACAA CCCCCTCAGC TCCAAGAGTG 1020  
 CCGGGAGGTG GGGGGCGGCG CATCCGCGGC CTGAGCTTG CTACCTCAGC CCATCCCCAC 1080  
 CACCCCTGAC ATCAGAGAAG CTGAGCTCAC CCCCATCTTG CCCTTCCTGT TCCTTGGCAA 1140  
 TGAGCAGGAT GCTCAGGACC TGGACACCAT GCAGCGGCTG AACATCGGCT ACGTCATCAA 1200  
 CGTCACCACT CATCTTCCCC TCTACCACTA TGAGAAAGGC CTGTTCAACT ACAAGCGGCT 1260  
 GCCAGCCACT GACAGCAACA AGCAGAACCT GCGGCAGTAC TTGAAGAGG CTTTGAAGT 1320  
 CATTGAGGAA GCTCACCAGT GTGGGAAGGG GCTTCTCATC CACTGCCAGG CTGGGGTGTG 1380  
 CCGCTCCGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA CCATGACTGA 1440  
 TGCTTATAAA TTGTCAAAAG GCAAACGACC AATTATCTCC CCAAACCTTA ACTTCATGGG 1500  
 GCAGTTGCTA GAGTTCGAGG AAGACCTAAA CAACGGTGTG ACACCGAGAA TCCTTACACC 1560  
 AAAGCTGATG GGCCTGGAGA CGGTTGTGTG ACAATGGTCT GGATGGAAAG GATTGCTGCT 1620  
 CTCCATTAGG AGACAATGAG GAAGGAGGAT GGATTCTGGT TTTTTCCTT TCTTTTTCCT 1680  
 TTGTAGTTGG GAGTAAAGTT TGTGAATGGA AACAACTTG GTTAAACACT TTATTTTAA 1740  
 CAAGTGTAAG AAGACTATAC TTTTGATGCC ATTGAGATTC ACCTTCACA AACTGGCCAA 1800  
 ATTAAGGAGG TTAAGAAAGT AATTTTTCCT AAGCCCAACC ATTAATAAT TAATACAAC 1860  
 TGGTTCTCC CCCTTTTCC TTFAAGCTA NTTGTAAAA GTTATGAG

Seq ID NO: 130 Protein sequence:  
 Protein Accession #: NP\_009138.1

1 11 21 31 41 51  
 MPPSLDDRV VVALSRPVRP QDLNLCLDSS YLGSANPGSN SHPPVIATTV VSLKAANLTY 60  
 MPSSSGSARS LNCGCSASG CTVATYDKDN QAQTQAJAAG TTTTATGTST TCPANQMVNN 120  
 NENTGSLSPS SGVGSFVSGT PKQLASIKI YPNDLAKKMT KCSKSHLPQ GPVIIDCRPF 180

MEYNKSHIQG AVHINCADKI SRRRLQQGKI TVLDLISCRE GKDSFKRIFS KEHVYDENT 240  
NEPSRVMPFSQ PLHIVLESLEK REGKEPLVLK GGLSSFKQNH ENLCDNSLQL QECREVGGA 300  
SAASSLLQP IPTTPDJENA ELTPILPLF LONEQDAQDL DTMQRLNIGY VINVTTHPL 360  
YHYEKGLFNY KRLPATDSNK QNLRQYFEEA FEFIEEAHQK GKGLLIHCQA GVSRSATIVI 420  
AYLMKHTRMT MTDAYKFVKG KRPIHPNLN FMGQLLEFEE DLNNGVTPRI LTPKLMGVET 480  
VV

Seq ID NO: 131 DNA sequence

Nucleic Acid Accession #: NM\_005409.3

Coding sequence: 94-378 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | |  
TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60  
CAACAGCAAC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120  
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180  
TGCTTTTGA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240  
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAAT 300  
AAGGACAAC GATGCTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360  
GAAAGAAAG ATTTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420  
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480  
AGACTTTTCT ATGGTTTGT GACTTTCAAC TTTGTACAG TTAAGTGAAG GATGAAAAGT 540  
GGGTGAAAAG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAAATCCA 600  
CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660  
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCCTAC TTGTGTATT ATACATTCAT 720  
GCATTTCTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780  
GAGAACATT CTCTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840  
CTGTGGTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900  
CACTATGTG TGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAATACAC ACTCTTTCC 960  
CCAAATATCA GTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTGTGTTTGT 1020  
TTTATAACCA ATTCATTAAT TGAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080  
TGGGATACTG GCAACAGTGC ACATATTTC TAACCAAATT AGCAGCACCG GTCTTAATTT 1140  
GATGTTTTTC AACTTTTAT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200  
TGTACTTTTT GTTTTGATCC GTTTGTATA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260  
TACAAAATGT TTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320  
AATCACTTTT ACTTTTGTG ATCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380  
TTGTTTCATG CTATATACTG TAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440  
GTCATTTTTT TCTCTAATA ACTACCACAA CCTTTCTTTT TAAAAAAA AAA

Seq ID NO: 132 Protein sequence:

Protein Accession #: NP\_005400.1

1 11 21 31 41 51  
| | | | |  
MSVKGMAIAL AVILCATVVQ GPPMFKRGRG LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60  
EVIITLKENK GQRLNPKSK QARLIKKVE RKNF

Seq ID NO: 133 DNA sequence

Nucleic Acid Accession #: NM\_012342

Coding sequence: 373-1155 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | |  
CTGGCGGGG CGGGAGCTGC GGCGGATACC CTTCGGTGCT GTGGAGACCC TACTCTCTTC 60  
GCTGAGAACG GCCGCTAGCG GGGACTGAAG GCCGGGAGCC CACTCCGAC CCGGGGCTAG 120  
CGTGCCTCCC TAGAGTCGAG CGGGGCAAGG GAGCCAGTGG CCGCCGACGG GGGACCGGGA 180  
AATCTTCTG GGCTCTTGA GAGCCCTGTA GCGCGCTCC ATGCTCCGGC AGCGGCCCGA 240  
AACCAGCCC CGCGCTGAC GGAGCCCGCC GCTCCGGCA GGGCCCATGC CTTGCGCGCT 300  
CCGGGGGTGC TAGTGCCGC CGAGCCGGGG CTCCGGAAGC CGGCGGGGGC GCGCGGCCG 360  
TGGGGGGCT CAATGGATCG CCACTCCAGC TACATCTTCA TCTGGCTGCA GCTGGAGCTC 420  
TGGCCCATGG CCGTGCTGCT CACCAAAGGT GAAATTCGAT GCTACTGTGA TGCTGCCAC 480  
TGTTAGCCA CTGGTTATAT GTGTAATCT GAGCTCAGCG CTTGCTCTC TAGACTTCTT 540  
GATCTCAGA ACTCAAATTC CCACTCACC CATGGCTGCC TGGACTCTCT TGCAAGCAGC 600  
ACAGACATCT GCCAAGCCAA ACAGGCCCGA AACCACTCTG GCACCAACAT ACCACATTG 660  
GAATGCTGTC ATGAAGACAT GTGCAATTAC AGAGGGCTGC ACGATGTTCT CTCTCTCTCC 720  
AGGGGTGAGG CCTCAGGACA AGGAAACAGG TATCAGCATG ATGGTAGCAG AAACCTTATC 780  
ACCAAGGTGC AGGAGCTGAC TCTTCCAAA GAGTTGTGGT TCCGGGACG GGTCTATTGC 840  
GTGCCCATTT CTGGAGGGCT GATTTTAGTG TTGCTTATTA TGTGGCCCT GAGGATGCTT 900  
CGAAGTGAAA ATAAGAGGCT GCAGGATCAG CGGCAACAGA TGCTCTCCCG TTGCACTAC 960  
AGCTTTACG GACACCATT CAAAAAGGGG CAGGTTGCAA AGTTAGACTT GGAATGCATG 1020  
GTGCCGGTCA GTGGGACGA GAACCTGCTG CTGACCTGTG ATAAAATGAG ACAAGCAGAC 1080  
CTCAGCAACG ATAAGATCT CTGCTTGT TACTGGGGCA TGTACAGTGG GCACGGGAAG 1140  
CTGGAATTCT TAGACGGAG TCTTATCTGA ACTACACTTA CTGAACAGCT TGAAGGCCTT 1200  
TTGAGTTCTG CTGGACAGGA GCACCTTATC TGAAGACAAA CTCAATTAAT CATCTTGAG 1260  
AGACAAAATG ACCTCTGCAA ACAGAATCTT GGATATTTCT TCTGAAGGAT TATTTGCACA 1320  
GACTTAAAT CAGTAAATG TGTATTTTGC TTTTAAAAAT ATAAAAAGCA AAGAGAAGAC 1380  
TTGTACACA CTGTACACG GGTATTGTG ATCCAAGGA GCTGGAATTG AGTACCTAAA 1440

TAAACAAAAA TGTGCCCTAT GTAAGCTTCT ACATCTTGAT TTATTGTAAA GATTTAAAAA 1500  
AAATATATAT ATTTTGTCTG A

Seq ID NO: 134 Protein sequence:  
Protein Accession #: NP\_036474.1

1 11 21 31 41 51  
MDRHSSYIFI WLQLELCAMA VLLTKGEIRC YCDAAHCVAT GYMCKSELSA CFSRLLDPN 60  
SNSPLTHGCL DSLASTTIDIC QAKQARNHSG TTIPTLECC EDMCNRYRLH DVLSPPRGEA 120  
SGQGNRYQHD GSRNLITKVQ ELTSSKELWF RAAVIAVPIA GGLILVLLIM LALRMLRSEN 180  
KRLQDQRQQM LSLRHYSHFG HHSKKGQVAK LDLECMVPVS GHENCCLTCD KMRQADLSND 240  
KILSLVHWGM YSHGKLEFV

Seq ID NO: 135 DNA sequence  
Nucleic Acid Accession #: NM\_001627.1  
Coding sequence: 64-1815 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
CGGGACGACG CCCCTCCTG CGGCGTGGAC TCCGTCACTG GCCCACCAG AAGGAGGAGG 60  
AATATGGAAT CCAAGGGGGC CAGTTCCTGC CGTCTGCTCT TCGCCTCTT GATCTCCGCC 120  
ACCGTCTTCA GGCCAGGCCT TGGATGGTAT ACTGTAAAT CAGCATATGG AGATACCAAT 180  
ATCATACCTT GCCGACTTGA CGTACCTCAG AATCTCATGT TTGGCAAATG GAAATATGAA 240  
AAGCCCGATG GCTCCCCAGT ATTTATTGCC TTCAGATCTT CTACAAAGAA AAGTGTGCAG 300  
TAGGACGATG TACCAGAATA CAAAGACAGA TTGAACCTCT CAGAAAACCTA CACTTTGTCT 360  
ATCAGTAATG CAAGGATCAG TGATGAAAAG AGATTGTGTG GCATGCTAGT AACTGAGGAC 420  
AAGGTGTTTG AGGCACCTAC AATAGTCAAG GTGTTCAGC AACCATCTAA ACCTGAAATT 480  
GTAAGCAAAG CACTGTTTCT CGAAACAGAG CAGCTAAAAA AGTTGGGTGA CTGCATTTC 540  
GAAGACAGTT ATCCAGATGG CAATATCACA TGGTACAGGA ATGGAAGAGT GCTACATCCC 600  
CTTGAAGGAG CGGTGGTCAT AATTTTAAAA AAGGAAATGG ACCCAGTGAC TCAGCTCTAT 660  
ACCATGACTT CCACCCCTGA GTACAAGACA ACCAAGGCTG ACATACAAAT GCCATTACCC 720  
TGCTCGGTGA CATATTATGG ACCATCTGGC CAGAAAACAA TTCATTCTGA ACAGGCAGTA 780  
TTTGATATTT ACTATCCTAC AGAGCAGGTG ACAATACAAG TGCTGCCACC AAAAAATGCC 840  
ATCAAAGAAAG GGGATAACAT CACTCTTAAA TGCTTAGGGA ATGGCAACCC TCCCCAGAG 900  
GAATTTTGT TTTACTTACC AGGACAGCCC GAAGGAATAA GAAGCTCAAA TACTTACACA 960  
CTGATGGATG TGAGGCGCAA TGCAACAGGA GACTACAAGT GTTCCCTGAT AGACAAAAAA 1020  
AGCATGATTG CTCAACAGC CATCACAGTT CACTATTGG ATTTGTCTTT AAACCCAAAGT 1080  
GGAGAAGTGA CTAGACAGAT TGGTGATGCC CTACCCGTGT CATGCACAAT ATCTGTAGC 1140  
AGGAATGCAA CTGTGGTATG GATGAAAGAT AACATCAGGC TTCGATCTAG CCCGTCATT 1200  
TCTAGTCTTC ATTATCAGGA TGCTGGAAAC TATGTCTGCG AAAGTGTCT GCAGGAGGTT 1260  
GAAGGACTAC AGTAAAGAGA GTCAATTGACT CTCATTGTAG AAGGCAAAACC TCAATAAAAA 1320  
ATGACAAAGA AAAGTATCC CAGTGGACTA TCTAAACAA TAATCTGCCA TGTGGAAGGT 1380  
TTTCCAAAGC CAGCCATTCA GTGGACAATT ACTGGCAGTG GAAGCGTCAT AAACCAAACA 1440  
GAGGAATCTC CTATATTAA TGGCAGGTAT TATAGTAAAA TTATCATTTT CCCTGAAGAG 1500  
AATGTTACAT TAAGTATCC AGAACACGAT GAGGCAGACG AGATAAGTGA TGAAGACAGA 1560  
GTCTCTGCTA TAAGTATCC AGAACACGAT GAGGCAGACG AGATAAGTGA TGAAGACAGA 1620  
GAAAAGGTGA ATGACACAGC AAAACTAATT GTGGGAATCG TTGTGGTCT CCTCCTTGGT 1680  
GCCCTGTTG CTGGTGTCTG TACTGGCTG TACATGAAGA AGTCAAAGAC TGCATCAAAA 1740  
CATGTAACA AGGACCTCGG TAATATGGA GAAAAACAAA AGTTAGAAGA AAACAATCAC 1800  
AAAAGTGAAG CTTAAGAGAG AAAGTCTCT AGTTGTCCAG AGATAAAAAAT CATATAGACC 1860  
AATTGAAGCA TGAACGTGGA TTGTATTAA GACATAAACA AAGACATTGA CAGCAATTCA 1920  
TGGTTCAAGT ATTAAGCAGT TCATTCTACC AAGCTGTAC AGGTTTTCAG AGAATTATCT 1980  
CAAGTAAAC AAATGAAAT TTAAATACAAA CAATAAGAAC AAGTTTGGC AGCCATGATA 2040  
ATAGGTGATA TGTGTGTTT GGTTCATTT TTTTCCGTA AATGTCTGCA CTGAGGATTT 2100  
CTTTTGGTT TGCTTTTAT GTAAATTTT TACGTAGCTA TTTTATACA CTGTAAGCTT 2160  
TGTCTGGGA GTTGTGTTA ATCTGATGTA TAATGTAATG TTTTATTTT AATTGTTTAT 2220  
ATGGATAATC TGAGCAGGTA CATTCTGAT TCTGATTGCT ATCAGCAATG CCCCAAACTT 2280  
TCTCATAAGC ACCTAAACCC CAAAGGTGGC AGCTGTGAA GATTGGGGAC ACTCATAATTG 2340  
CCCTAATTAA AAAGTGTGAT TTTATCACA AGGGAGGGGA GGCCGAGAGT CAGACTGATA 2400  
GACACCATAG GAGCCGACTC TTTGATATGC CACCAGCGAA CTCTCAGAAA TAAATCACAG 2460  
ATGCATATAG ACACACATC ATAATGGTAC TCCCAACTG ACAATTTTAC CTATTCTGAA 2520  
AAAGACATAA AACAGAATT

Seq ID NO: 136 Protein sequence:  
Protein Accession #: NP\_001618.1

1 11 21 31 41 51  
MESKGASSCR LFLCLISAT VFRPLGWYT VNSAYGDTH IFCRLDVPQN LMFQKWKYEK 60  
PDGSPVFI AF RSTTKSVQY DDVPEYKDR LNLSENYT LSI SNARISDEKR FVCM LVTEDN 120  
VFEAPTIVKV FKQPSKPEIV SKALFLETEQ LKLLGDCISE DSYPDGNITW YRNGKVLHPL 180  
EGAVVHFKK EMDPVTQLYT MTSTLEYKIT KADIQMPFTC SVTYYGPSQK KTIHSEQAVF 240  
DIYYPTEQVT IQVLPPKNAL KEGDNITLKC LGNGNPPPEE FLFYLPQPE GIRSSNTYTL 300  
MDVRRNATGD YKCLSLDKKS MIASTAITVH YLDLSLNSFG EVTRQIGDAL PVSCITISASR 360  
NATVVWMKDN IRLRSSPSFS SLHYQDAGNY VCETALQEV EGLKRESLTL IVEGKPBQKM 420  
TKKTDPSGLS KTIHCHVEGF PKPAIQWTT GSGSVINQTE ESPYINGRY SKIISPEEN 480

VTLTCTAENQ LERTVNSLNV SAISIPEHDE ADEISDENRE KVNDQAKLIV GIVVGLLLAA 540  
LVAGVYVWLY MKKSKTASKH VNKDLGNMEE NKKLEENNHK TEA

5 Seq ID NO: 137 DNA sequence  
Nucleic Acid Accession #: XM\_030559  
Coding sequence: 1-119 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51  
| | | | |  
ATGAACCGCA GCCACCGGCA CGGGGCGGGC AGCGGCTGCC TGGGCACTAT GGAGGTGAAG 60  
AGCAAGTTTG GAGCTGAATT TCGTCGGTTT TCGCTGGAAA GATCAAAACC TGGAAAATTT 120  
GAGGAGTTT ATGGATTACT ACAACATGTT CATAAGATCC CCAATGTTGA CGTTTGGTA 180  
GGCTATGCAG ACATCCATGG AGACTTACTA CCTATAAATA ATGATGATAA TTATCAGAAA 240  
15 GCTGTTCAA CGGCCAATCC ACTGCTTAGG ATATTTATAC AAAAGAAGGA AGAAGCAGAC 300  
TACAGTGGCT TTGGTACAGA CACGCTAATA AAGAAGAAGA ATGTTTAAAC CAACGTATTG 360  
CGTCCTGACA ACCATAGAAA AAAGCCACAT ATAGTCATTA GTATGCCCCA AGACTTTAGA 420  
CCTGTGCTT CTATTATAGA CGTGGATATT CTCCCAGAAA CGCATCGTAG GGTACGTCIT 480  
TACAAATACG GCACGGAGAA ACCCCTAGGA TTCTACATCC GGGATGGCTC CAOTGTCAGG 540  
20 GTAACACCAC ATGGCTTAGA AAAGGTTCCA GGGATCTTTA TATCCAGGCT TGTCACAGGA 600  
GGTCTGGCTC AAAGTACAGG ACTATTAGCT GTTAATGATG AAGTTTGA AGTTAATGGC 660  
ATAGAAGTTT CAGGGAAGAG CCTTGATCAA GTAACAGACA TGATGATTGC AAATAGCCGT 720  
AACCICATCA TAACAGTGAG ACCGGCAAAC CAGAGGAATA ATGTTGTGAG GAACAGTCGG 780  
ACTTCTGGCA GTTCCGGTCA GTCTACTGAT AACAGCCTTC TTGGCTACCC ACAGCAGATT 840  
25 GAACCAAGCT TTGAGCCAGA GGATGAAGAC AGCGAAGAAG ATGACATTAT CATTGAAGAC 900  
AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCTAATA CTGAGAGCCT GGAGTCATTA 960  
ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATCCCTC TAATGAAGTG 1020  
AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTTG AAACACATGC TCCAGATCAA 1080  
30 AAACCTCTAG AAGAAGATGG AACAATCATA ACATTATGA

Seq ID NO: 138 Protein sequence:  
Protein Accession #: XP\_030559

35 1 11 21 31 41 51  
| | | | |  
MNRSHRHGAG SGCLQTM EVK SKFGAEFRRF SLERSKPGKF EEFYGLLQHV HKIPNVDVLV 60  
GYADIHGDLI PINDDNYHK AVSTANPLLR IFIQKKEAD YSAGTDIL KKKNVLTNVL 120  
RPDNHRKKPH IVISMPQDFR PVSSHDVDI LPETHRRVRL YKYGTEKPLG FYIRDGSSVR 180  
40 VTPHGLEKVP GIFISRLVPG GLAQSTGLLA VNDEVLEVNG IEVSGKSLDQ VTDMMIANSR 240  
NLITVRPAN QRNNVVRNSR TSGSSGQSTD NSLLGYFQOI EPSFEPEDED SEEDDIIED 300  
NGVPQQPKA VNTESLESLE TQIELSFESG QNGFIPSNEV SLAAIASSN TEFETHAPDQ 360  
45 KLEEDGTII TL

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All  
5 publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1                   1.       A method of detecting a breast cancer-associated transcript in a cell  
2       from a patient, the method comprising contacting a biological sample from the patient with a  
3       polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence  
4       as shown in Tables 1-25.
- 1                   2.       The method of claim 1, wherein the biological sample comprises  
2       isolated nucleic acids.
- 1                   3.       The method of claim 2, wherein the nucleic acids are mRNA.
- 1                   4.       The method of claim 2, further comprising the step of amplifying  
2       nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1                   5.       The method of claim 1, wherein the polynucleotide comprises a  
2       sequence as shown in Tables 1-25.
- 1                   6.       The method of claim 1, wherein the polynucleotide is immobilized on  
2       a solid surface.
- 1                   7.       The method of claim 1, wherein the patient is undergoing a therapeutic  
2       regimen to treat breast cancer.
- 1                   8.       The method of claim 1, wherein the patient is suspected of having  
2       breast cancer.
- 1                   9.       An isolated nucleic acid molecule consisting of a polynucleotide  
2       sequence as shown in Tables 1-25.
- 1                   10.      The nucleic acid molecule of claim 9, which is labeled.
- 1                   11.      An expression vector comprising the nucleic acid of claim 9.
- 1                   12.      A host cell comprising the expression vector of claim 11.

- 1                   13.    An isolated polypeptide which is encoded by a nucleic acid molecule  
2   having polynucleotide sequence as shown in Tables 1-25.
- 1                   14.    An antibody that specifically binds a polypeptide of claim 13.
- 1                   15.    The antibody of claim 14, further conjugated to an effector component.
- 1                   16.    The antibody of claim 15, wherein the effector component is a  
2   fluorescent label.
- 1                   17.    The antibody of claim 15, wherein the effector component is a  
2   radioisotope or a cytotoxic chemical.
- 1                   18.    The antibody of claim 15, which is an antibody fragment.
- 1                   19.    The antibody of claim 15, which is a humanized antibody
- 1                   20.    A method of detecting a breast cancer cell in a biological sample from  
2   a patient, the method comprising contacting the biological sample with an antibody of claim  
3   14.
- 1                   21.    The method of claim 20, wherein the antibody is further conjugated to  
2   an effector component.
- 1                   22.    The method of claim 21, wherein the effector component is a  
2   fluorescent label.
- 1                   23.    A method for identifying a compound that modulates a breast cancer-  
2   associated polypeptide, the method comprising the steps of:  
3                   (i) contacting the compound with a breast cancer-associated polypeptide, the  
4   polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least  
5   80% identical to a sequence as shown in Tables 1-25; and  
6                   (ii) determining the functional effect of the compound upon the polypeptide.
- 1                   24.    A drug screening assay comprising the steps of



- 2 (i) administering a test compound to a mammal having breast cancer or a cell  
3 isolated therefrom;
- 4 (ii) comparing the level of gene expression of a polynucleotide that selectively  
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25 in a  
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control  
7 cell or mammal, wherein a test compound that modulates the level of expression of the  
8 polynucleotide is a candidate for the treatment of breast cancer.